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Drosophil Drosophil Sequence

Run on:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 1835;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1835; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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Sequence 1 from Patent WO02062977.
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Location/Qualifiers
1. 1835
/organism="Homo sapiens"
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(c) 1993 - 2005 Compugen Ltd.
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                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Conteat: MGC help deak
Email: cgapba-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Center
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Conteat: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 50 Row: k Column: 10.
Location/Qualifiers
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                 Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/note="Lipase_GDSL; Region: GDSL-like
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Qy 963 ACGTGGTGGAGGTCAGGTGGCTAGCCTGTACCAGGCCAAGGCGGGAAATGTGCCA 1022		
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4106 CAGTGGGCCGCAAGACTACCTCCAACAACTTCACCCACGGCGAGCCAAACTCAAGTGCC	ò	
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1563 CTCCAATGAGCCTGCGCACTGTGGCCCTCTAG 1594	₹ dd	423 GTGACTTCCT 2489 GTGACTTCCT
Db 4346 CTCCAATGAGCCTGCGCACTGTGGCCCTCTAG 4377	ò	
RESULT 4	ପ୍	 2549 TCCGACCAGC
LOCUS AX417817 3648 bp DNA linear PAT 18-JUN-2002 DEFINITION Sequence 1 from Patent WO0231161.		
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	λ ₀ α	603 TTGGAGGGA 2669 TTGGAGGGA
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.	č	663 ACCCITACCI
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L Patent: WO 0231161-A 1 18-APR-2002; BAYER AG (DE)	ò	
FEATURES Location/Qualifiers 1. 3648 13648	q _O	
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72.98:	ò	843 GGGTCAACGA
i, Indels		2909 GGGTCAACGA
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2188 31GGTGCTGCAGCCCTTCTTCCAGAACATCCAGCTCCCTGTCCTGGC---- 273 2548 SCAGACATCAAAGTGGTGGCCGCCCTGGGTGACTCTCTGACTACAGGAGTGG 542 AATGGGAACTIGGAGACTCACACACTGCCCAACAITCTGAAGAAGTICA 662 TICCTTGGCTTCTCTACCAGCACCTGGGAGAGGACAGGAGGATAAATGTGG 722 ACTIGIGATA TACTGAGA ATCCGGAGGCCCACTGGCCACGGAATATG 902 BATACGTCCTTCTTTGCCCCAGACTGCATCCACCCAAATCAGAAATTCCACT 2308 168 TGACCCTGCGGGAGAACTCCCAAGAGCTAGCCAGGCTGGAGGCCTTCAGCC 2128 218 302 362 422 482 782 842 TTCAGCACATCCAACAGGCCTGGACATCCTCTGAGGGGCTCCCAAGGGCTTTCGTCA 962 --GAGCAGCATGCGCGAGCTGGTGGGCGCTAGCGCTATGACACGCAGGAGG TGTGTACAGAGTGGAAGGCTTCCAATAGTGTTCCAACCTCTGTCCACCAGC TTCCTGGGAAACCCAGACAAGTGCCCAGTGCAGCCAGCCCA-----GGAATAGTAACTACACGTACCCCATCAAGCCAGCCATTGAGAACTGGGGCA TIGTGTACAGAGGAGGCTTCCAATAGTGTTCCAACCTCTGTCCACCAGC STGCCCAGAGTCCTGGTCAACCTCGTGGACTTCCTGAACCCCACTATCATGC TGAGAGCAGAGATGCCCATCACCTGTCCCACTCAGAATGAGCCCTTCCTGA GCCCCGACATCAACCTGGAAAAACTGGAAGCTGGTCACACTCTTCATTG aggeccagactragggacargecageccraggecraggecgaa AACTITGITCACCATCTCCGCAATGCCTTGGACGTCCTGCATAGAG-

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Bessenger RNAs expressed in intestine of adult but not baby
rabbits. Isolation of cognate cDNAs and characterization of a novel
brush border protein with esterase and phospholipase activity
J. Biol. Chem. 268 (17), 12901-12911 (1993)
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Mamalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                        Direct Submission
Submitted (25-UUN-1992) WERNER BOLL, Dept. of Biochemistry
Swiss Federal Institute of Technology, ETH Zentrum,
Swiss Federal Institute of Zuerich, CH-8092, Switzerland
Universitatestrasse 16, Zuerich, CH-8092, Switzerland
Location/Qualifiers
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FNPSIFGFFSTGTLEETAGFNVAVEEARARDMPAQARDLVBRMKASTEINLEMDWKLIT
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(bases 1 to 4608)

Delagebeaudeut, C., Gassama-Diagne, A., Nauze, M., Ragab, A., Li, R. Capdevielle, J., Ferrara, P., Fauvel, J. and Chap, H.

Sctopic epididymal expression of guinea pig intestinal phospholipase B. Possible role in sperm maturation and activat: J. Biol. Chem. 273 (22), 13407-13414 (1998)
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Delagebeaudeuf, C., Gassama-Diagne, A., Nauze, M., Ragab, A.,
Capdevielle, J., Ferrara, P., Fauvel, J. and Chap, H.
Direct Submission
Submitted (30-JAN-1998) INSERM unite 326, Hopital Purpan,
31059, France
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B (PLB) mRNA, complete cds.
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/strain="Crl:(BFA)BR"
/db xref="taxon:10141"
/tisue type="intestine"
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/db_xref="GI:3172337"
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Rattus norvegicus (Norway rat)
Rattus norvegicus (Lordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Submitted (22-UUI-1995) Hiromasa Tojo, Osaka University Medical
Submitted (22-UUI-1995) Hiromasa Tojo, Osaka 2-2 Yamada-oka, Suita
School, Molecular Physiological Chemistry; 2-2 Yamada-oka, Suita
School, Japan (E-mail:htojo@mr-mbio.med.osaka-u.ac.jp,
Tel:06-879-3283(ex.3283), Fax:06-879-3288)
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                                       4590 bp mRNA linear ROD for phospholipase B, complete cds
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QGGHCTALLPAQSTCSCLRHFPSSPYJQELKKYTWNLQSDNSELSYOENTQREDFAV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                      3644 AGACTGGAAGCTGATTACACTCCTCATCGGGAACAACGACCTGTGTCTTTACTGTGAGGA
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Tojo,H. and Hasegawa,A.
NEW PHOSPHOLIPASE AND DNA CC
Patent: JP 1997248190-A 1 22
TOJO HIROMASA, TONEN CORP
OS Rattus Sp. (rat)
PN JP 1997248190-A/1
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E13935
E13935.1 GI:3252702
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NKHETFAVVEOFFESVELPLERFSFODSTTLALRINNSWMEVGRKDGTLARSKRT
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ADIKVIGAMODSLTAGNGAGSSPGNYLDVLTQYRGLGWSVGGDETIETTVTLAILIRE
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I ITVYTGGSNUCGSCNULARFSPQTFTDNIKTALDILHAEVPRAFWNWSVIETTPR
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NPELDFEKDWKLITVLFSNTSQCHLCSSDQQKRHLMKHMEMLSGVLDYLHREPPRAFV
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DFAVTVQPFFRNTFVPLDERGGLDLTFFSEDCFHFSVRGHAEMAIALMNNMLEPVGKK
TTSNNFTYNRTKLKCPSPENPFLYTVRNSQIILDKAKENSNTLYWAVPVAAVGGLVVG
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43.9%; Score 805.2; DB 10; Length
Best Local Similarity 77.1%; Pred. No. 1.6e-193;
Matches 994; Conservative 0; Mismatches 293; Indels
/tissue_type="small intestine"
36. .4388
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                                        /codon_start=1
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/protein_id="BAA23813.1"
/db_xref="GI:2696236"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                GCTCCACGACCAGGGGGGAAATGTGCCGTTGGCCGTTGGCTGTCCAGAAAAACTGCAGTTG
                                                                                                                                                                                                            CCTCAGACACTCGCAAAGCTCCCTGGAGGAAGCAAGAACTGAAGAAAGTGAACTGGAACT
                                                                                                                                                                                                                                              CCAGCATGGCATCTCCAGCTACTGGCACCAATACACACAGGGTGAGGACTTTGC
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Patent: WO 0231161-A 4 18-APR-2002;
BAYER AG (DE)
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Similarity 99.1%; Pred. No. 4.7e-135;
78; Conservative 0; Mismatches 5;
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        CTCTGAGGAGCTCCCAAGGGCTTTCGTCAACGTGG

    .583
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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AX417820
AX417820.1 GI:21522938
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PF 15-MAR-1996 JP 1996086022

PI TOJO HIROMASA, HASEGAWA AKIRA

PC C12M15/09, CO7121/04, C07K14/47, C12N5/10, C12N9/16, PC

C12N9/20//A61K38/46,

PC (C12N5/10, C12R1:91), (C12N9/16, C12R1:91), (C12N9/20, C12R1:91);

CC strandedness: Double;

CC topology: Linear;

Location/Qualifiers

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/organism='Rattus sp.'
/tissue type='lleum'
36. .4397
/product='phospholipase precursor'
36. .125
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/product='phospholipase'.
Location/Qualifiers
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Pred. No. 1.6e-193;
0; Mismatches 293;
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/organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"
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Best Local Similarity 77.1%;
Matches 994; Conservative C
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                                                                                                                                      1309 CAACATGCTGGAACCAGTGGGCCGCAAGACTACCTCCAACAACTTCACCCACAGCCGAGC

1401 CAACATGCTGGAACCAGTGGGCCGCAAGACTACCTCCAACATTCACCCACAGCCGAGC
                                                                                                                                                                                                                                                                       GCTCCCGGGCTGGAGGCCCCCGGGGGGCTCTACTGGGCTGTCCCAGTGCCAG
                        CTTCCAAAACACACTCACCCCACTGAACGAGAGAGAGGGACACTGACCTCACCTTCTTCTC
                                                                                        CGAGGACTGTTTTCACTTCTCAGACCGCGGCATGCCGAGATGGCCATCGCACTCTGGAA
                                                                                                                                                                                                        CAAACTCAAGTGCCCCTCTCCTGAGGCCCTTACCTCTACACCCTGCGGAACAGCCGATT
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      CTTCCAAAACACACTCACCCCACTGAACGAGAGAGGGGACACTGACCTCACCTTCTCTC
                                                                       CGAGGACTGTTTTCACTTCTCAGACCGCGGGCATGCCGAGATGCCCATCGCACTCTGGAA
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0231161-A 7 18-APR-2002;
BAXER AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.0%; Score 440.2; DB 6; 99.1%; Pred. No. 9.5e-101; Live 0; Mismatches 4;
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Sequence 7 from Patent WO0231161.
AX417823 AX417823.1 GI:21522941
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                                                CTTCACTGCCCTCTGCCCCAGCCACTCCCGGCCACCAGGACATGCTTCAATGCCTGGTGC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                      AGGIGCICIACIGGCCIGICCCAGIGGCAGGGGGAGICGGCCIIGIGGGCAICGICAICG 284
                                                                                                                                                                                                                                                                                                                                                         GGACAGTGGTCTGGAGGTGCAGGAGGTGGCCGGAGGAAGATCCTCCAATGAGCCTGC 224
                                                                                                                                                                                                                                                                                                                                                                                                                           GCACTGGTGCCCTCTAGGCCCGGGGGTGGGTCCTCACCCTAAACTCCCTATAGCCACCCT 164
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
CTTCACCGCCCTCTGCCCCAGCCACTCCCGGCCACCAGAACATCATGCCTGGTGC
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CQ715991
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PE Corporation (NY) (US)
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Location/Qualifiers
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                                        1655 CCAGCCACTCCCGGCCACCAGGACATGCTTCAATGCCTGGTGCCATAGGAAGCCCAAGGG 1714
                                                                                            1715 ACAGTCACAACTTCTTGGGGCCTTCTTCCAGGCCTATGCTCCTGGAATGGATACA 1774
Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                      GTGGTGGGCATCATCGGACAGTGGTCTGGAGGTGCAGGAGGTGGCCGGAGGGAAGAT
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PE Corporation (NY) (US)
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/db_xref="taxon:9606"
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Sequence 3 from Patent WO02062977.
AX711964
AX711964.1 GI:29787749
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                                                                                                                                                                        TTTAAATAAAGTCCAAAGCTATTTA 1
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Best Local Similarity 98.8
Matches 414; Conservative
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Direct Submission
Submitted (09-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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         PRI 07-NOV-2001
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (07-NOV-2001) Department of Genetics, Washington Bubmitted (07-NOV-2001) Department of Genetics, Missouri 63108, On Aug 9, 2001 this sequence version replaced gi:13431259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108,
AC074011 180465 bp DNA linear PRI 07-1
Homo sapiens BAC clone RP11-780J6 from 2, complete sequence.
AC074011
                                                                                                                                                                                                                                                                         2 (bases 1 to 180465)
Paulson,E., Cotton,M. and Lohmeyer,A.
The sequence of Homo sapiens BAC clone RP11-780J6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                        1 (bases 1 to 180465)
Sulston, J.B. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Submitted (09-AUG-2001)
University, 4444 Forest
5 (bases 1 to 180465)
                                                                       GI:15144519
                                                                                                                                                                                                                                                                                                                                                                                                                                              MO 63108, USA
4 (bases 1 to 180465)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 180465)
Waterston, R.H.
                                                                                                        sapiens (human)
                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                        AC074011.5
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       AC074011
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MARPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for Genetics, Washington University, St. Louis
MCB-herson, Department of Genetics, Washington University, St. Louis
MC. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

The RPCI-11 human BAC library was made from the blood of one male The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at the Roswell Park Cancer Institute

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102351 GCTGAAGAAGCCCCCGAGGTGCTCTACTGGGCTGTCCCCAGTGGCAGCGGGAGTCGGCCTT 102410
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23401. .23688
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1689.
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Matches 414; Conservative
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                                        of this
base
                                    The clone sequenced to the right is AC022076. Actual start clone is at base position 1 of RP11-780J6; actual end is at position 180465 of RP11-780J6.

Location/Qualifiers

1. 180465

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8849. .9043
(http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1407. .11443
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1888. .11997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="L2"
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13779. .14059
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32. . 651
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3140. .3189
                                                                                                                                                                                                                                                                                                   -y-09. .5050
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3365. .6677
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5099. 15154

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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION RESULT 14 AC022076

ACCESSION

VERSION

1682

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1622

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces arbitrary daps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                       Worley, K.C.
Direct Submission
Submitted (08-JAN-2003) Human Genome Sequencing Center, Department
Submitted (08-JAN-2003) Human Genetics, Baylor College of Medicine, One
Daylor Plaza, Houston, TX 77030, USA
On Apr 28, 2002 this sequence version replaced gi:16117882.
   Submitted (26-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 163595)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: HABR
Center project name: HABR
Center clone name: RP11-34L7
------- Summary Statistics
Sequencing vector: M13,
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 156062 bases at least Q40
Consensus quality: 160990 bases at least Q30
Consensus quality: 160990 bases at least Q20
Estimated insert size: 163913; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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2569: contig of 2569 bp in length
2570 4826: gap of unknown length
4827 4926: gap of unknown length
4827 4926: gap of unknown length
4827 8967: contig of 2157 bp in length
8968 12664: gap of unknown length
9068 12664: gap of unknown length
2765 17841: contig of 357 bp in length
7764: gap of unknown length
7765: gap of unknown length
7765: gap of unknown length
7766: gap of unknown length
7776: gap of unknown length
7777: gap of unknown length
7778: gap of unknown length
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Pred. No. 2.4e-85;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine
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mol type="genomic DNA"
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Best Local Similarity 97.1%;
Matches 409; Conservative (
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                                                                                                                                                                                                                                                                                                                                      COMMENT
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RS Muzny, D.M., Adama; C., Adio-Oduola, B., Ali-Osman, F. M. Allen, C., Alian, C., Barbara, J., Benton, J., Binege, H.C., Arel, E., Brown, M., Bryant, N. B., Bouck, J., Carter, G., Brieva, M., Brown, E., Brown, M., Bryant, N. Bubok, J., Carter, C., Burrell, K.L., Byra, N.C., Burd, N.C., Coxten, G., Elice, A., Cavole, M., Dathorne, S.R., David, N.C., Davila, M.L., Davis, C., Davy-Carroll, Dathorne, S.R., David, R., Delgado, C., Davy-Carroll, Dathorne, S.R., David, R., Delgado, C., Davy-Carroll, Dathorne, S.R., David, R., Delgado, C., Davy-Carroll, Dathorne, C., Bord, R., Delane, Y.C., Bernart, C., Bortin, M., Douthwaite, K.J., Deraper, H., Dugan-Roofa, S., Dubrin, K.J., Barnhart, C., Edgar, D., Flagg, N., Ford, J., Forder, S., Hartis, K., Hart, M., Hale, S., Hamilton, K., Gorzell, J. H., Guevara, W., Gunaratne, P., Hale, S., Haille, B., Harris, C., Harris, K., Hart, M., Hale, S., Hamilton, K., Gorzell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hallins, B., Harris, C., Harris, K., Hart, M., Hale, S., Surface, J., Howard, S., Hober, J., Johnson, R., Jollyee, S. G., Joudah, S., Garcia, A., Homson, R., Jollyee, S. G., Gorzell, J., Liu, W., Louiseged, H., Li, J., Liu, M., Louiseged, H., J., Li, J., Li, Z., Lichtearge, C., Lieu, J., Liu, M., Louiseged, H., J., Li, Z., Lichtearge, C., Lieu, J., Liu, M., Louiseged, M., Massey, E., Manniey, E., Martin, R., Martin, R., Martina, R., Martin, R., Martina, R., Martin, C., Miner, Z., Mitcher, J., Luicer, R., Luice, R., Luicer, R., Luicer, R., Luicer, R., Scherer, R., Scott, G., Saver, G., Grade, R., Rojas, A., Rojas, A.,
   ACUZZU76

163595 bp DNA linear HTG 08-JAN-2003

Homo sapiens chromosome 3 clone RP11-34L7, WORKING DRAFT SEQUENCE,

11 unordered pieces.
                                                                                                                                                                                                                                        CTTCAATGCCTGGTGCCATAGGAAGCCCAGGGGACAGTCACAACTTCTTGGGGCCTGGGC 1741
                                                                                                     TCCCTATAGCCACTCTTCACCGCCCTCTGCCCCAGCCACTCCCGGCCACCAGGACATG 1681
                                                                                                                                                                                                                                                                                                                                                                          Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC022076.13 GI:20335454
HTG; HTGS PHASEL; HTGS DRAFT.
HOMO sapiens (human)
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2 (bases 1 to 163595)
Worley, K.C.
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3

TITLE JOURNAL REFERENCE AUTHORS

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Sequencing Center, (MISC), (MI
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SPERPPLYTLANSQILDFDKAEEPSNALYWAVPVAAIGGLAVGILGYMLWRTVKFVQQE
EEEEDTIPNTSVTQDAVSEKRIKAGN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 65 Row: 1 Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 26024306. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by biopsy."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 TGTCTTGTAGGAAAAACTGCAGTTGCTTAAGACACTCCCAAAACCTCACAGCGATGCAGG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 Geracargadecreadaderreceaarcacrereceaacerrecegaaracerra 220
      institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1086 AACTGAAGAAAGTGAACTGGAACCTCCAGCATGGCATCTCCAGTTTCTCCTACTGGCACC
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                               USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                old mouse. Taken by biopsy.
/clone_lib="NCI_CGAP_Mam2"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Hsieh, F.,

Biatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunatane, P.H., Richards, S.,

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Villalon, D.K., Murany, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Ranchez, A., Whiting, M., Madan, A., Woung, A.C., Shevchenko, Y.,

Butferd, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanius, D.E.,

Schnetch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,

Generation and initial analysis of more than 15,000 full-length
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                                                                                                                                                                                                                                                                                                                                      91056 TGGGGTGGGCATCATCGGGACAGTGGTCTGNAGGTGCAGGAGAGGTGGCCCGCAAGGAAG 91115
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                             90936 CCTCCACAGAGAGCCCTTACCTCTACACCCTGCGGAACAGCCGATTGCTCCCAGACCAG
                                                                                                                                    GCTGAAGAAGCCCCCGAGGTGCTCTACTGGGCTGTCCCAGTGGCAGCGGGAGTCGG-CCT
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Proc. Natl. Acad. Sci. U.S.A. 9
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Direct Submission
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Copyright (c) 1993 - 2005 Compugen Ltd.
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	(without alignments) 11367.434 Million cell updates/sec
Title:	US-09-778-961-1
Perfect score:	1835
Sequence:	r ccycagccaactrgctgacaaaaaaaaaaaaaaaaa 1835
Scoring table:	IDENTITY NUC
Searched:	Gapop 10.0 , Gapext 1.0 4390206 segs, 2959870667 residues

8780412 Total number of hits satisfying chosen parameters: DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

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geneseqn2000s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Abq82234 Human pho	Aad52634 Human lip	Ado18837 Human lip	Aad52626 Human lip	Adh13733 Human ENZ	Adh42430 Novel hum	Adn61816 Human cDN	Ado18836 Human lip	Abx97050 Human NOV	Abq77623 Human lip	Abg77624 Human lip	Aad37410 Human pho	Abx97048 Human NOV	Adh42426 Novel hum	Adn61812 Human cDN	Aat91874 Rat phosp	Aah99765 Human pro	Aba08297 Human pho	Aad37411 Human pho	Abl89761 Human pol
SUMMARIES		di	ABQ82234	AAD52634	AD018837	AAD52626	ADH13733	ADH42430	ADN61816	ADO18836	ABX97050	ABQ77623	ABQ77624	AAD37410	ABX97048	ADH42426	ADN61812	AAT91874	AAH99765	ABA08297	AAD37411	ABL89761
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ALIGNMENTS

Human phospholipase protein encoding cDNA SEQ ID NO:1. Human; phospholipase; enzyme; chromosome 2; gene; ss. /*tag= a 176. 1594 /*tag= b /product= "phospholipase" 1595. 1835 Location/Qualifiers 1. .175 ABQ82234 standard; cDNA; 1835 BP. 28-JAN-2002; 2002WO-US002302. 08-FEB-2001; 2001US-00778961. 16-DEC-2002 (first entry) (PEKE) PE CORP NY. WO200262977-A2 Homo sapiens 15-AUG-2002. ABQ82234; Key 5'UTR 3'UTR CDS RESULT 1 ABQ82234

Di Francesco V, Beasley EM; WPI; 2002-682698/73. P-PSDB; ABP53556. Yan C, Ketchum KA,

New human phospholipase proteins, useful for the development of human therapeutics and diagnostic compositions, drug screening assays, tissue typing and pharmacogenomic analysis.

Claim 4; Fig 1A; 95pp; English.

The present sequence encodes a human phospholipase protein (I) located on chromosome 2. (I) can be used for identifying agents that modulate its chromosome 2. (I) can be used for identifying agents that modulate its function or activity where the agent is useful for treating a disease or condition mediated by a the human phospholipase protein. (I) peptides can condition mediated by a the human phospholipase protein. (I) peptides can condition mediated by a the human phospholipase protein. (I) peptides can information of the peptide sequences, to raise antibodies or to elicit information of the peptide sequences, to raise antibodies or to elicit immune response, as reagents in assays that determine the levels of protein in biological fluids, and as markers for tissues where the corresponding protein is expressed. Nucleotide sequences encoding (I) can be used as probes, primers and chemical intermediates in biological can be used in the identification of therapeutic proteins and may serve as models or targets for the development of human therapeutic agents that compliants phospholipase activity in cells and tissues that express the phospholipase, such as in kidney, blood, lung, brain glioblastomas, correspondent colon or leukocytes

Seguence 1835 BP; 458 A; 549 C; 474 G; 354 T; 0 U; 0 Other;

099 600 99 540 9 GACCCTGGACCTGAGAGCAGAGATGCCCATCACCTGTCCCACTCAGAATGAGCCCTTCCT 360 480 480 540 300 420 420 240 240 TCCCTTAGGTGCCCAGAGTCCTGGTCAACCTCGTGGACTTCCTGAACCCCACTATCATGC 120 180 180 9 9 gerceaecaacaecarcarcaaagreereeceecereerearerracaecae gggagcircaaccaaactrocagigaacciaaccaacaictiggaggggaacroricaaag CATTGGAGGGATGGGAACTTGGAGACTCACCACACTGCCCAACATTCTGAAGAAGTT CAGTGACTTCCTGTGTACAGGGTTCGAATAGTTTCCAATAGTGTTCCAACCTCTGTCCACCA CGAGCTGGTGGGGTTAGGCACACGCAGGAGGACTTCTCTGTGGTGCTGCAGCC CTTCTTCCAGAACATCCAGCTCCCTGGCGCTTGAACCACTTGGAAGCAAAACAGA GGCAGGTGTTCCTGGGAAACCCAGACAAGTGCCCAGTGCAGCAGCAGCAGCATGCG CTGCAACTTTGTTGACCATCTCCGCCAATGCCTTGGACGTCCTGCATAGAGAGCTTT Сарв ; 0 Length 1835; Indels ; . 0 DB query Match 100.0%; Score 1835; Best Local Similarity 100.0%; Pred. No. 0; Matches 1835; Conservative 0; Mismatches 481 541 601 361 421 421 481 541 601 241 181 181 241 301 301 361 ,н ч 61 61 121 121

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1620 1680 1680 1560 1620 1500 1500 1320 1380 1320 1140 1140 1020 1020 1080 960 780 840 840 900 900 960 CICCCIAIAGCACICICITCACCGCCCTCIGCCCCAGCCACCCGGCCACCAGGACAT gerrepariscerregrisecerrassassecerassassecresses accagigggcgcacaagaciaccicaagaaciicacccacagcggaggcaaacicaagig cecercicergagacecritaceacecragasacagasacagarracressagacea gecneaagaccccccaaggrecrcracragacrcracragragagacrcg ACTCACCCCACTGAACGAGGGGGACACTGACCTCCACCTTCTTCTCCGAGGACTGTTT GCACCAATACACACACAGGGGGGACGTTGCGGTTGTGGGGGCCTTTCTTCCAAAACAC TCACTICICAGACGCGGGGCAIGCCGAGATGGCCAICGCACTCTGGAACAACAIGCTGGA TGTTCAGCACCACCAACAGGCCCTGGACATCCTCTGAGGAGCTCCCAAGGGCTTTCGT CAACGIGGIGGAGGICAIGGAGCIGGCIAGCCIGIACCAGGGCCAAGGCGGGAAAIGIGC cangeriegeagericagaacaacriecacriegecacacacacacaacageagaaa GCAAGAACTGAAGAAAGTGAACTGGAACCTCCAGCATGGCATCTCCAGTTTCTCCTACTG GGCAGCGGAAGGGCCAGAGCTAGGGACATGCCAGGCCCAGGCCTGGGACCTGGTAGAGCG AATGAAAAACAGCCCCGACATCAACCTGGAGAAAGACTGGAAGCTGGTCACACTCTTCAT TGGGGTCAACGACTTGTGTCATTACTGTGAGAATCCGGAGGCCCACTTGGCCACGGAATA 1801 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1835 1741 1501 1561 1561 1621 1621 1681 1691 1741 1441 1261 1321 1381 1381 1201 1201 1261 1321 1141 1021 1021 1081 1081 1141 781 841 901 901 196 961 721 781 721 g g ò ò g 8 셤 g 셤 ò 셤 ò 셤 à ò 셤 g ò ď ò g 8 ò g ò ద ò g Š g 8 g 셤 8 à

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Human; lipid-associated molecule; LIPAM; cardiovascular disorder; stroke; arteriovenous fistula; atherosclerosis; hypertension; Raynaud's disease; aneuryem; congestive heart failure; thrombophlebitis; anglina perctoris; ischaemic heart disease; rheumatic heart disease; peptic cosophagitis; ansusea; peptic ulcer; fatty liver; Fabry's disease; Crohn's disease; diabetes mellitus; hyperlipidaemia; hypercholesteroleemia; epilepsy; autoimmune disorder; inflammatory disorder; neurological disorder; kuru; acquired immunodeficiency syndrome; anaemia; Alzheimer's disease; asthma; dementia; prion disease; Creutzfeldt-Jakob disease; leukaemia; cancer; adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; gene therapy; protein replacement therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baughn MR, Burford N, Reddy R;
Yao MG, Arvizu CS, Lu Y, Gandhi AR;
Imar J, Lal PG, Lu DAM, Lee EA, Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Human mature LIPAM-9 protein"
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"Human LIPAM-9 protein"
                                                                                                                                               Human lipid-associated molecule (LIPAM)-9 cDNA.
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25-WAY-2001; 2001US-0293736F.
01-UJN-2001; 2001US-0295346P.
06-JUL-2001; 2001US-0303404P.
24-MUG-2001; 2001US-0314754P.
22-JAN-2002; 2002US-0351262P.
29-MAR-2002; 2002US-0351262P.
                                                                        AAD52634 standard; cDNA; 4424
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Walia NK, Das D, Nguyen DB,
Griffin JA, Elliott VS, Ramk
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                                                           AAD52634
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The present invention relates to novel human lipid-associated molecules (LIPAM) and polynucleotides encoding such proteins. Sequences of the invention are useful for treating diseases or conditions associated with decreased expression of functional LIPAM. The antagonist is useful for treating a disease or condition associated with the overexpression of treating a disease or condition associated with the overexpression of treating a disease (a secondary of the overexpression of the conditional LIPAM. They are useful for diagnosing, treating or preventing cardiovascular disorates (e.g. arteriovenous fistula, atherosclerosis, hypertension, Raynaud's disease, aneuryems, varicose veins, congestive heart failure, thrombophlebitis, angina pectoris, ischaemic heart disease (e.g. retury liver, Fabry's disease, daucher's disease, diabetes disorders (e.g. fatty liver, Fabry's disease, Gaucher's disease, diabetes complitues, hyperlipidaemia, hypercholesterolaemia,, autoimmune disorders or inflammatory disorders (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's disease, or prion diseases such as kuru or Creutzfeldt-Jakob disease), neurological disorders (e.g. epilepsy, dementia, Altheimer's disease, or prion diseases such as kuru or Creutzfeldt-Jakob disease) or cancers (e.g. adenocarcinoma, leukaemia, leukaemia, myeloma or sarcoma). They are also used in gene therapy and protein replacement therapy. The present sequence is human therapy.
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                                                                                                             * human lipid-associated molecule (LIPAM) proteins and polynucleotide
eful for diagnosing, treating or preventing cardiovascular disorders
.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCAGCCAACTTTGTTCACCATCTCCGCAATGCCTTGGACGTCCTGCATAGAG-----
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  Swarnakar A;
Kable AE,
                                                                                                                                                                                                                               Claim 74; Page 168-169; 171pp; English.
Tribouley CM,
                                           2003-120797/11.
Yue H, Yang J,
                                                                 P-PSDB; AAE34448
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op Oy	3085 GCTCCGACCAGCAGACATCAAAGTGGTGGCCGCCCTGGGTGACTTCTGACTACAGCAGT 3144 541 GGGAGCTCGACCAAACAACTCCAGTGACCTACCCACATCTTGGAGGGACTCTTGGAG 600	δ; A	1621 CTCCCTATAGCCACTCTCT
qa	-6 -6	ð í	1681 GCTTCAATGCCTGGTGCC
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हें ह	661 CAACCCTTACCTCCTTGGCTTCTCTACCAGCACGGGAGGGGACAGGACTAAATGT 720 	음 &	4345 CTTCTTCCAGGCCTATGC 1801 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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8 8	, 5 = 1	XX	ADO18837; 12-AUG-2004 (first entry)
qa X		% X B X	Human lipid-associated mole lipid-associated molecule;
g &		<u> </u>	antidiabetic; cytostatic; dantiinflammatory; thyromim gastrointestinal; hepatotry antiparkinsonian; antibact
යි .		*	virucide; uropathic; antiri nootropic; LIPAM agonist; neurodegenerative disorder
දු දු		i K K	muscular disorder; myotoni Grave's disease; cancer; l
જે ત	1081 GCAAGAACTGAAGAAGTGAACTGGAACTCCAGCATCTCCAGTTTCTCCTACTG 1140 	KW KW	luminioserinal allergy, gastrointestinal Goodpasture's syndrome; in protozoal; helminthic; car
8 & 8	1141 GCACCAATACACACACGTGAGGACTTTGCGGTTGTGGTGCAGCCTTTCTTCCAAAACAC 1200 	¥ X 8 X	hepatic disease; cirinosis Homo sapiens.
8 &	1201 ACTCACCCACTGAACGAGAGGGGACACTGACCTCACCTTCTTCTCCGAGGACTGTTT 1260	NY XX	WO2004044165-A2. 27-MAY-2004.
g 8		XFX	10-NOV-2003; 2003WO-US0355
A q		# # # #	13-NOV-2002; 2002US-04261 12-DEC-2002; 2002US-04332: 07-MAR-2003; 2003US-04531
γο dg	398		13-MAR-2003; 2003US-04548 24-APR-2003; 2003US-04654 24-APR-2003; 2003US-04656
8	1381 CCCTCTCTGAGAGCCCTTACCTCTACACCTGCGGAACAGCCGATTGCTCCCAGACCA 1440	*	(INCY-) INCYTE CORP.
8 &	13985 CCCCICLOGRANGCCCCCGAGGTGCTCTATGGGTGTCCCAGTGGCAGCGGGAGTCGGCCT 1500 1441 GGCTGAAGAAGCCCCCGAGGTGCTCTATGGGTGTCCCAGTGGCAGCGGGAGTCGGCCT 1500	I I I	Jiang X, Becha SD, Bull. Emerling BM, Gietzen KJ, Lee SY, Marquis JP, Mur
g &			
d d		TA	New LIPAM polypeptides, u disorders associated with
& 점	1561 TCCTCCAATGAGCCTGCGCACTGTGGCCCTCTAGGCCCGGGGGTGGGT		

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cule; LIPAM; neuroprotective; relaxant; antithyroid; tic; dermatological; immunosuppressive; romimetic; antiallergic; crebroprotective; attotroprotective; attotroprojic; nephrotropic; anticonvulsant; ibacterial; antiparasitic; fungicide; protozoacide; ibacterial; antiparasitic; fungicide; protozoacide; antirheumatic; cardiant; cardiovascular; anti-HIV; antirheumatic; cardiant; cardiovascular; anti-HIV; order; parkinson's disease; Alzheimer's disease; otonic dystrophy; catatonia; endocrime disorder; er; leukaemia; cervical; breast cancers; r; scleroderma; systemic lupus erythematosus; r; scleroderma; systemic lupus erythematosus; inal disorder; crohn's disease; renal disorder; cardiovascular disorder; atherosclerosis; hosis; transgenic animal; gene; ds; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                loch SA, Chang H, Chawla NK, Elliott VS;
J, Hafalia AJA, Jackson AA, Kable AE, Khare R;
mrage J, Swarnakar A, Yang YG;
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th abnormal expression or activity of LIPAM, e.g.
gical, cardiovascular disorders, cancer and/or
CTTCACCGCCTCTGCCCCAGCCACTCCCGGCCACAGACAT 1680
                                                                                                                                            4344
                                                                                                                                                                                          CTCCTGGAATGGATACATTTAAATAAGTCCAAAGCTATTTA 1800
                                                                                             CATAGGAGGCCAGGGGACAGTCACAACTTCTTGGGGCCTGGG 1740
                                                                                                                                                                                                                   lecule (LIPAM) gene SeqID32.
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215P.
127P.
1801P.
5495P.
5619P.
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This invention relates to novel human lipid-associated molecules (LIPAM)
and the DNA sequences which encode them. The invention may be useful for
the production of compounds with a neuroprotective, relaxant,
antithyroid, antidiabetic, cytostatic, dermatological, immunosuppressive,
antinflammatory, thyromimetic, antiallergic, cerebroprotective,
cartinflammatory, thyromimetic, antiallergic, cerebroprotective,
cartinflammatory, thyromimetic, antiallergic, cerebroprotective,
cartinflammatory, thyromimetic, antiallergic, cerebroprotective,
contropartion antibacterial, antiparasitic, fungicide, protozoacide,
contropic activity acting as LIPAM agonists or antagonists. In addition,
the disclosed sequences may be useful for gene therapy. The invention may
contropic activity acting as LIPAM agonists or antagonists. In addition,
the disclosed sequences may be useful for gene therapy. The invention may
contropic activity acting as LIPAM agonists or antagonists.
The disclosed sequences may be useful for gene therapy. The invention may
contropic activity acting as LIPAM agonists of LIPAM, such as
nuscular disorders (for example myotonic dystrophy, catatonia),
chiesase), muscular disorders (for example myotonic dystrophy, catatonia),
chiesample scleroderma, systemic lupus erythemanological disorders
(for example scleroderma, systemic lupus erythemanological disorders
(for example scleroderma, systemic lupus erythemanological disorders
(for example doodpasture's syndrome), infections (for example viral,
chacterial, fungal, parasitic, protozoal, helminthic), cardiovascular
disorders (for example atherosclerosis), or hepatic diseases (for example
compounds that specifically bind to and modulate the activity of LIPAM.
The polynucleotides can be used to create humanised animals or transgenic
compounds that specifically and conset humanised animals or transgenic
confounds. lipid-associated molecule (LIPAM) gene of the invention. õ . 2

Sequence 4512 BP; 1115 A; 1266 C; 1182 G; 949 T; 0 U; 0 Other;

'n, 2733 2793 GACCAATATGCTTGAACCACTTGGAAGCAAAACAGAGAGACCCTGGACCTGGAGAGCAT 3033 240 2914 TGCCCCAGACTGCATCCACCCAAATCAGAAATTCCACTCCCAGGCTGGCCAGAGCCCTTTG 2973 3094 CACGTACCCCATCAAGCCAGCCATTGAGAACTGGGGCAGTGACTTCCTGTGTACAGAGTG 3153 ------GCTTGAACCACTTGGAAGCAAAACAGAACCCTGGACCTGGACCTGAGAGT 324 GCCCATCACCTGT.CCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTA 384 CACGTACCCCATCAAGCCAGCCATTGAGAACTGGGGCAGTGACTTCCTGTGTACAGAGTG 444 445 GAAGGCTTCCAATAGTGTTCCAACCTCTGTCCACCAGCTCCGACCAGCAGAGATCAAAGT 504 9 CTGCAGCCAACTTTGTTGACCATCTCCGCAATGCCTTGGACGTCCTGCATAGAGAGCTTT CTGCAGCCAACTTTGTTCACCATCTCCGCAATGCCTTGGACGTCCTGCATAGAG-----TCCCTTAGGTGCCCAGAGTCCTGGTCAACCTCGTGGACTTCCTGAACCCCACTATCATGC 2680 -----AddrdcccAdAdrccrddrcaAccrcdrdaAcrrccrdaAccccAcrarcArdc GGCAGGTGTTCCTGGGAAACCCAGACAAGTGCCAGTGCAGCAGGCCAGAGCAGCATGCG CGAGCTGGTGGGGTCAGGCCGCTATGACACGCGGAGGACTTCTCTGTGGTGCTGCAGCC Gaps DB 12; Length 4512; 2; Indels 119; Query Match
88.7%; Score 1627.8;
Best Local Similarity 93.6%; Pred. No. 0;
Matches 1778; Conservative 0; Mismatches 2626 2734 3034 61 2794 241 2854 2974 385 121 181 274 274 325 셤 g g g 셤 ઠે ð δ ે 8 8 8 8 & 8 ે

3333 1044 3753 1104 1513 3393 3513 3573 3633 3693 1164 1217 1393 1453 4173 4233 ATCGGGACAGTGTCTGGAGGTGCAGGAGAGGTGGCCGGAGGGAAGATCCTCCAATGAGC 1573 624 744 804 864 984 3214 GGIGGCCCCCIGGGIGACTCTCTGACTACAGCAGTGGGAGCTCGACCAAACAACTCCAG 3334 GACTCACACCACACTGCCCAACATTCTGAAGAAGTTCAACCCTTACCTCTGCTTGGCTTCTC CCTGGAGAAGACTGGAGCTGGTCACTCTTCATTGGGGTCAACGACTTGTCTCATTA 3574 CTGTGAGAATCCGGAGGCCCACTTGGCCACGGAATATGTTCAGCACATCCAACAGGCCCT GGCTAGCCTGTACCAGGGCCAAGGCGGGAAATGTGCCATGCTGGCAGCTCAGAACAACTG CACTTGCCTCAGACACTCGCAAAAGCTCCCTGGAGAAAGGCAAGAACTGAAAAAGTGAAACTG ----AGAGAGGGGACACTGACCTCCTTCTTCCCGAGGACTGTTTTCACTTCTCAGAC CCCGAGGTGCTCTACTGGGCTGTCCCCAGTGGCGGGGGGGCTCGGCCTTGTGGGGGGGATC 3274 TGACCTACCCACATCTTGGAGGGACTCTTGGAGCATTGGAGGGGGAGGATGGGAACTTGGA GACTCACACACACTGCCCAACATTCTGAAGAAGTTCAACCCTTACCTCCTTGGCTTCTC TACCAGCACCTGGGAGGGGACAGCAGGACTAAATGTGGCAGCGGAAGGGGCCAGAGCTAG 3394 TACCAGCACCTGGGAGGGGACAGGACTAAATGTGGCAGCGGAAGGGGGCCAGAGCTAG GGACATGCCAGCCCAGGCCTGGACCTGGTAGAGCGAATGAAAAACAGCCCCGACATCAA 3454 GGACATGCCAGCCCAGGCCTGGGACCTGGTAGAGCGAATGAAAAACAGCCCCGACATCAA 3514 CCTGGAQAAGACTGGAAGCTGGTCACACTCTTCATTGGGGTCAACGACTTGTGTCATTA GGACATCCTCTGAGGAGCTCCCAAGGGCTTTCGTCAACGTGGAGGTCATGGAGCT CTTTGCGGTTGTGGTGCAGCCTTTCTTCCAAAACACACTCACCCCACTGAACG-----3934 CTGCAGAGAGGGGACACTGACCTCTCTTCTCCGAGGACTGTTTTCACTTCTCAGAC 4054 AAGACTACCTCCAACAACTTCACCCACAGCCGAAGCCAAACTCAAGTGCCCCTCTCCTGAG AGCCCTTACCTCTACACCCTGCGGAACAGCCGACTGCTCCCCAGACCAGGCCTGAAGCC TGACCTACCCACATCTTGGAGGGACTCTTTGGAGCATTGGAGGGGATGGGAACTTGGA CTGTGAGAATCCGGAGGCCCACTTGGCCACGGAATATGTTCAGCACATCCAACAGGCCCT GGACATCCTCTCTGAGGAGCTCCCAAGGGCTTTCGTCAACGTGGTGGAGGTCATGGAGCT GGCTAGCCTGTACCAGGGCCAAGGCGGAAATGTGCCATGCTGGCAGCTCAGAACAACTG GAACCTCCAGCATGCCATCTCCAGTTTCTCCTACTGGCACCAATACACACAGCGTGAGGA CGCGGGCATGCCGAGATGGCCATCGCACTCTGGAACAACATGCTGGAACCAGTGGGCCGC 3994 CGCGGGCATGCCGAGATGGCCATCGCACTCTGGAACAACATGCTGGAACCAGTGGGCCGC AGCCCTTACCTCTACACCCTGCGGAACAGCCGATTGCTCCCAGACCAGGCTGAAGAACC GTGGTGGGCATC CCCGAGGTGCTCTACTGGGCTGTCCCAGTGGCAGCGGGAGTCGGCCT 3154 685 265 745 805 1045 625 3634 3814 3874 1514 505 865 925 985 3694 3754 1105 1165 1218 1334 1394 4114 1454 요 g 요 원 ద ò ò Š 셤 ઠે g ઠે à ò g ò g à g à 셤 ઠે ઠે 음 ∂ 유 ð g ઠે 셤 ⋧ 셤 ò 셤 ठ us-09-778-961-1.rng

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                                                                                                                                                                                                                                         Human; lipid-associated molecule; LIPAM; cardiovascular disorder; stroke; arteriovenous fistula; atherosclerosis; hypertension; Raynaud's disease; anneurysm; congestive heart failure; thrombophlebitis; angina pectoris; ischaemic heart disease; peptic oseophagitis; gastrointestinal disorder; lipid metabolism disorder; Crohn's disease; nausea; peptic ulcer; fatty liver; Fabry's disease; Gaucher's disease; diabetes mellitus; hyperlipidaemia; hypercholesterolaemia; epilepsy; autoimmune disorder; inflammatory disorder; neurological disorder; kuru; acquired immunodeficiency syndrome; anaemia; Alzheimer's disease; asthma; demontia; prion disease; Creutzfeldt-Jakob disease; leukaemia; cancer; adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; gene therapy; protein replacement therapy; gene; ss.
                                                                                 GTGCCATAGGAAGGCCCAGGGGACAGTCACATCTTGGGGCCTGGGCTTCTTCCAGGCC 1753
                                                 CTCTCTTCACCGCCCTCTGCCCAGCCACTCCCGGCCACCAGGACATGCTTCAATGCCTG 1693
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ATCGGGACAGTGGTCTGGAGGTGCAGGAGAGGTGGCCGGAGGGAAGATCCTCCAATGAGC 4293
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/product= "Human mature LIPAM-1 protein"
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                                                                                                                     TATGCTCCTGGAATGGATACATTTAAATAAAGTCCAAAG 1792
                                                                                                                              "Human LIPAM-1 protein"
                                                                                                                                                                                                                               Human lipid-associated molecule (LIPAM)-1 cDNA.
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The present invention relates to novel human lipid-associated molecules CC (LIPPAM) and polymucleotides encoding such proteins. Sequences of the invention are useful for treating diseases or conditions associated with invention are useful for treating a disease or condition associated with the overexpression of teneting a disease or condition associated with the overexpression of teneting a disease or condition associated with the overexpression of teneting a disease or condition associated with the overexpression of tenetional LIPPAM. They are useful for diagnosing, treating or preventing cradiovascular disorders (e.g. arteriovancus fistula, atherosclerosis, cardiovascular disease, aneurysms, varicose veins, congestive hypertension, Raymand's disease, aneurysms, varicose veins, congestive or rheumatic heart disease, gastrointestinal disorders (e.g. peptic or rheumatic hauty liver, Pabry's disease, Gaucher's disease diabetes disorders (e.g. fatty liver, Pabry's disease, Gaucher's disease diabetes con inflammatory disorders (e.g. acquired immunodeficiency syndrome, or inflammatory disorders (e.g. acquired immunodeficiency syndrome, con inflammatory disorders (e.g. acquired immunodeficiency syndrome, or inflammatory disorders (e.g. acquired immunodeficiency syndrome, con inflammatory disease), neurological disorders (e.g. stroke, epilepsy, dementia, Alzheimer's disease, or prion diseases used in gene con creatizeldt-Jakob disease) or cancers (e.g. adenocarcinoma, leukaemia, cherapy and protein replacement therapy. The present sequence is human therapy. The present sequence is human constraints.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human lipid-associated molecule (LIPAM) proteins and polynucleotides, useful for diagnosing, treating or preventing cardiovascular disorders (e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCAGCCAACTTTGTTGACCAATCCCGCAATGCCTTGGACGCTCCTGCATAGAGAGCTTT
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e EA, Lee
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Arvizu CS, Lu Y, Gandhi
Lal PG, Lu DAM, Lee EA,
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Pred. No. 0;
0; Mismatches 3; Indels 192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Swarnakar A;
                                                                                                                                                                                                                                                                                                                                                                                                                   rang YT, Yue H, Azimzai Y, Baughn MR, B
Walia NK, Das D, Nguyen DB, Yao MG, Arv
Griffin JA, Elliott VS, Ramkumar J, Lal
Yue H, Yang J, Tribouley CM, Kable AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 66; Page 158-159; 171pp; English.
                                                             18-MAY-2001; 2001US-0292242P.
25-MAY-2001; 2001US-0293726P.
01-UUN-2001; 2001US-0295346P.
06-UUL-2001; 2001US-0303404P.
24-AUG-2001; 2001US-0313754P.
22-JAN-2002; 2002US-0351262P.
29-MAR-2002; 2002US-036999P.
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Best Local Similarity 90.2%;
Matches 1799; Conservative (
17-MAY-2002; 2002WO-US015688.
                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-120797/11.
P-PSDB; AAE34440.
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1143 ACCANTACACACACGGTGAGACTTTGCGGTTGTGGTGAGCCTTTCTTCCAAACACAC 3993 1203 TCACCCACTGAGACTTTGCCGTTGTGGTGAGCCTTTCTTCCCAAACACAC 3993 1203 TCACCCACTGACACACGGGAACTTTGCCGGTTGTTGTTCCGAGGACTTTTC 1653 1203 TCACCCCACTGACACGGGAACACTGACCACCTCTTCTTCTCCGAGGACTGTTTTC 1653 1204 TCACCCCACTGACACGGGACACACTGACCACCACTCTTCTCTCCGAGGACTGTTTTC 1653 1205 TCACCCCACTGACACGGGGACACACTGACCACCACTCTTCTCCGAGGACTGTTTTC 1653 1207 TCACCCCACTGACACGGGGACACACTGACCACCACCACTCTTCTCCGAGGACTGTTTTC 1653 1208 ACTTCTCAGACGGGGGACACCCCACACCACCCACACCCACACACA	RESULT 5 ADH13733 ID ADH13733 standard; DNA; 4311 BP. XX AC ADH13733; XX DT 11-MAR-2004 (first entry) XX DE Human ENZM enzyme gene sequence SeqID86. XX XX Muman; ENZM; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; XX
169	183 TGADADA CAGCCCCGACATCAACCTGGAGAAAGACTGGAAGCTGGTCACACTCTTCATTG 1 1 1 1 1 1 1 1 1

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CAACGTGGTGGAGGTCATGGAGCTGGCTTGTACCAGGGCCAAGGGGGAAATGTGC 1020
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                    GGGAGCTCGACACACACACAGACCTACCCACATCTTGGAGGGGACTCTTGGAG
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CAGTGACTTCCTGTGTACAGAGTGGAAGGCTTCCAATAGTGTTCCAACCTCTGTCCACCA
                                                                 GCTCCGACCAGCAGACATCAAAGTGGTGGCCCCCTGGGTGACTCTCTGACTACAGT
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                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to novel human enzymes (ENZM) and the genes which concode them. The invention may be useful for the development of compounds with a cytostatic, antiarteriosclerotic, anticonvulsant, nootropic, with a cytostatic, antiarteriosclerotic, antiallargic, nourcoprotective, cerebroprotective, anti-HV, antiallargic, notropic, antifilfammatory or thyromimetic activity or for gene therapy. The invention may therefore be useful in diagnosing, treating and preventing invention may therefore be useful in diagnosing, treating and preventing concerces conditions associated with the decreased expression or alterosclerosis), neurological (for example epilepsy, Huntington's atherosclerosis), neurological (for example epilepsy, Huntington's atherosclerosis), immune/inflammatory (for example syndrome) disorders convenient of the example Hypothyroidism, Cushing's syndrome) disorders or infections. These are also useful in assessing the effects of sequences of ENZM, the present sequence is that of a gene which encodes a constant of the expression of interior and amino acid the entry of the entr
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                                                                                                                                                                                                                                                                                                            New human enzymes (ENZM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant ENZM expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or infections.
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                                                                                                                                                     Khare R, Kable AE, Lee SY, Hafalia AJA, Chawla NK, Marquis JP; Ramkumar J, Wilson AD, Jin P, Hawkins PR, Bulloch SA, Swarnakar A; Elliott VS, Richardson TW, Mason PM, Baughn MR, Yue H, Becha SD; Tang YT, Batra S, Lu DAM, Bhatia UG, Burrill JD, Lee S, Blake JJ; Ho A, Zheng W, Gao J;
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Pred. No. 0;
0; Mismatches 2; Indels 128; (
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Best Local Similarity 92.8%;
Matches 1673; Conservative
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17-MAY-2002; 2002US-0381558P.
                                             29-APR-2003; 2003WO-US013821
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P-PSDB; ADH13664.
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                                                                                           GGAGTCGGCCTTGTGGGGGCATCATCGGGACAGTGGTCTGGAGGGGCGCAGGAGGTGCC
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                               CGGAGGAAGATCCTCCAATGAGCCTGCGCACTGTGGCCCTCTAGGCCCGGGGGTC
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04-JUN-2002; 2002US-0386515P.
06-JUN-2002; 2002US-0386555P.
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17-UUN-2002; 2002US-0389146P.
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19-UUN-2002; 2002US-0389146P.
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19-UUN-2002; 2002US-0389184P.
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23-CCT-2002; 2002US-042065P.
23-CCT-2002; 2002US-042065P.
23-CCT-2002; 2002US-042065P.
23-CCT-2002; 2002US-042065P.
23-CCT-2002; 2002US-042065P.
23-CCT-2002; 2002US-042095P.
23-CCT-2002; 2002US-042065P.
23-CCT-2002; 2002US-042065P.
23-CCT-2002; 2002US-042065P.
23-CCT-2002; 2002US-042065P.
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(CURA-) CURAGEN CORP.

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WPI; 2004-053467/05. P-PSDB; ADH42431.

New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, in chromosome mapping, tissue typing or in pharmacogenomics.

Claim 20; SEQ ID NO 983; 1503pp; English.

The invention relates to 566 new isolated human polypeptides and their encoding genes, sequences that are at least 95% identical to these or sequences comprising one or more conservative substitutions in these. The polypeptide, polymuclectide and antibodies against the polypeptides are useful in diagnosing, treating or preventing NoVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, alzheimer's disease, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, parkinson's disease, asthma, or fertility disorders. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicione, and pharmacogenomics. The polypeptides are also useful as vaccines. This sequence represents an example of the nucleic acid sequence of the invention.

us-09-778-961-1.rng

940 TIGGEGGCANGGACTICISTICATION TITLE	RESULT 7 ADN61816 ID ADN61816 standard; CDNA; 4425 BP. XX AC ADN61816; XX DT 01-JUL-2004 (first entry) XX DE Human CDNA encoding NOV24c. XX
So Sequence 4425 BP, 1083 A; 1238 C; 1180 G; 924 T; 0 U; 0 Other; Suerinca Similarity 88.64; Pred, No. 0; Suerinca 169; Conservative 88.64; Pred, No. 0; Suerinca 169; Conservative 88.64; Pred, No. 0; Suerinca 169; Conservative 88.64; Pred, No. 0; De 514 CTCCASCOCCASCOCCACACTCCCCANTCCTTCCACACTCCTCCANTCATC 120 61 TCCCTTAGGTGCTTCTTCCCATTCCCTCCTCTCCTCCACCCCCTCTCTCATCCTC 2647 De 5294	

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cancer-associated cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease.
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02-APR-2001, 2
02-APR-2001, 2
04-APR-2001, 2
13-APR-2001, 2
13-APR-2001, 2
03-MAY-2001, 2
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03-MAY-2001, 2
15-MAY-2001, 2
16-MAY-2001, 2
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27-SEP-2001;
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                                    Homo sapiens
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New NOVX polypeptides and nucleic acid molecules useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

P-PSDB; ADN61817.

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Claim 17; SEQ ID NO 85; 786pp; English.

The invention relates to an isolated polypeptide (designated NOVX, or NOV1-NOV127) comprising a sequence selected from 178 fully defined amino acid sequences (and their mature forms, variants and fragments). Also included are an isolated nucleic acid molecule encoding NOVX, a vector comprising the nucleic acid, a cell comprising the vector, methods for determining the presence or amount of the polypeptide or the nucleic acid molecule in a sample, methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject, a method for identifying an apent that binds to the above polypeptide or nucleic acid molecule in a first mammalian subject, a method for identifying an apent that binds to the above polypeptide or identifying a potential therapeutic agent for subject, a method for identifying a potential therapeutic agent for use in the treatment of a pathology that is related to aberrant expression or physiological interactions of the polypeptide and a method for modulating correcting for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide and a method for modulating are useful for diagnosing, preventing or treating diseases such as are useful for diagnosing, preventing or treating diseases such as cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or parknison's disease, immune disorders, haematopoietic disorders, charmatomias, and other chronic diseases. These may also be used in chromosome mapping, tissue typing, preventive medicine and

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Ilpid-associated molecule, LIPAM; neuroprotective; relaxant; antithyroid; antidiabetic; cytostatic; dermatological; immunosupressive; antidiabetic; cytostatic; dermatological; immunosupressive; antiinflammatory; thyromimetic; antialergic; creptoprotective; gastrointestinal; hepatotropic; anticonvulant; antiparasitic; fungicide; protozoacide; virucide; uropathic; antipheumatic; cardiant, cardiovascular; anti-HIV; nootropic; LIPAM agonist; LIPAM antaqonist; gene therapy; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; muscular disorder; protozoacide; protozoacide; was muscular disorder; protozoacide; prot
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Hafalia AJA, Jackson AA, Ko
Je J, Swarnakar A, Yang YG;
Human lipid-associated molecule (LIPAM) gene SeqID31
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is JP, Murage J,
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13-MAR-2003; 2003US-0454801P.
24-APR-2003; 2003US-0465495P.
24-APR-2003; 2003US-0465619P.
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2002US-0433215P
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Marquis JP,
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Lee SY, N
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PPI; 2004-420307/39.
P-PSDB; ADO18815.
New LIPAM polypeptides, useful for diagnosing, preventing, and treating disorders associated with abnormal expression or activity of LIPAM, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and/or infections.

Claim 5; SEQ ID NO 31; 207pp; English

This invention relates to novel human lipid-associated molecules (LIPAM)
and the DNA sequences which encode them. The invention may be useful for
the production of compounds with a neuroprotective, relaxant,
antidiamatory, thyromimetic, dermatological, immunosuppressive,
antinflammatory, thyromimetic, antiallergic, cerebroprotective,
cartinflammatory, thyromimetic, antiallergic, cerebroprotective,
cartinflammatory, thyromimetic, antiallergic, cerebroprotective,
cartinflammatory, thyromimetic, antiallergic, fungicide, protozoacide,
cartinflammatory, antirheumatic, cardiant, cardiovascular, anti-HIV or
notropic activity acting as LIPAM agonists or antagonists. In addition,
the disclosed sequences may be useful for gene therapy. The invention may
be useful for diagnosing, preventing, and treating disorders associated
with an abnormal expression or activity of LIPAM, such as
cerebrated disorders (for example Parkinson's disease, Alzheimer's
disease), muscular disorders (for example myotonic dystrophy, catatonia),
catample leukaemia, cervical or breast cancers), immunological disorders
(for example scleroderma, systemic lupus erythematosus, allergies),
catample doodpasture's syndrome), infections (for example viral,
compounds that specifically bind to and modulate the activity of LIPAM.

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            sequence is that of a human
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 or
                                                           Sequence 4508 BP; 1108 A; 1256 C; 1190 G; 954 T; 0 U; 0 Other;
                                                                                          Length 4508;
 polynucleotides can be used to create humanised animals
                                                                                                                                                                                                                                                                             GCCAGGTGTTCCTGGGAAACCCAGACAAGTGCCCAGTGCAGCAGGCCA--
                                                                                                                       Indels
              animals to model human disease. The present sequence is lipid-associated molecule (LIPAM) gene of the invention.
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Mismatches
                                                                                          Score 1400;
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86.5%;
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Best Local Similarity 86.5
Matches 1705; Conservative
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NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer; hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine; human; gene; 88.
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2001US-0276000P.
2001US-0277331P.
2001US-0277321P.
2001US-0277321P.
2001US-0277321P.
2001US-0277321P.
2001US-0277833P.
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2001US-027338P.
2001US-027338P.
2001US-027338P.
2001US-027338P.
2001US-02899P.
2001US-0289852P.
2001US-0289852P.
2001US-0289858P.
2001US-0288342P.
2001US-0288342P.
2001US-0288342P.
2001US-0288342P.
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2001US-029833P.
2001US-029833P.
2001US-029889P.
2001US-0299303P.
2001US-0299303P.
2001US-0299303P.
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08-MAR. 2001; 200105-027422P.
08-MAR. 2001; 200105-027422P.
12-MAR. 2001; 200105-0275578P.
13-MAR. 2001; 200105-0275578P.
13-MAR. 2001; 200105-0275578P.
13-MAR. 2001; 200105-0275678P.
14-MAR. 2001; 200105-0275678P.
15-MAR. 2001; 200105-0276600P.
16-MAR. 2001; 200105-0276994P.
20-MAR. 2001; 200105-0276994P.
21-MAR. 2001; 200105-0277321P.
22-MAR. 2001; 200105-0277321P.
22-MAR. 2001; 200105-0277321P.
23-MAR. 2001; 200105-0277321P.
23-MAR. 2001; 200105-0277321P.
23-MAR. 2001; 200105-0277331P.
22-MAR. 2001; 200105-0277331P.
23-MAR. 2001; 200105-0277331P.
27-MAR. 2001; 200105-0277331P.
27-MAR. 2001; 200105-0277331P.
27-MAR. 2001; 200105-0277338P.
27-MAR. 2001; 200105-0279338P.
28-MAR. 2001; 200105-0279338P.
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                                                                                 Human NOV24c cDNA.
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18-JUN-2001;
19-JUN-2001;
19-JUL-2001;
31-JUL-2001;
16-JUL-2001;
11-SEP-2001;
12-SEP-2001;
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15-MAY-2001; 2
16-MAY-2001; 2
16-MAY-2001; 3
30-MAY-2001; 3
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04-APR-2001; 2
13-APR-2001; 2
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02-MAY-2001; 2
03-MAY-2001;
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02-APR-2001; 2
02-APR-2001; 2
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Trchangccnggraccanaganagcccagagagagagagagagagracaagracaaggccraaggcr 1742
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, 2001US-0332272P.

, 2001US-033184P.

, 2001US-0332034P.

, 2001US-0337426P.

, 2001US-0338092P.

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Zerhusen BD, Gu
Patturajan M, C
Fernandes ER, C
Spaderna SK, C
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/*tag= b /ncleotide polymorphism (SNP); leads to an /ncle= "Single nucleotide polymorphism (318 of the protein" Ala to Val substitution at position 1318 of the protein"
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                                                                                                                                                                                                                                                                                                                                                                                                               Human; lipase; chromosome 2; phospholipase B homologue; thyroid; brain; inflammatory disease; proliferative disease; infectious disease; clotting disorder; cancer; drug screening; mental disorder; Null dispositic reagent; clinical trial monitoring; cosmetic; nutriceutical; mutation detection; gene expression analysis; transgenic animal; noctropic; cytostatic; antiinflammatory; single nucleotide polymorphism; SNP; gene; therapy; gene; 8B.
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             GCCCCTCTCCTGAGGCCCTTAACACCTGCGGAAACAGCCGATTGCTCCCAGACC
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/product= "Human lipase NHL"
replace (1953, T)
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                                                                                                                                                                                                                                                                                                                                    ABQ77623 standard; cDNA; 4377
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P-PSDB; ABB09555.

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The invention relates to a novel human lippase (NHL, ABB09555, ABB09556)

CC and to nucleic acids encoding it (ABD77623, The NHL has

CC structural similarity with animal lippases, particularly phospholipase B.

cc structural similarity with animal lippases, particularly phospholipase B.

cc structural similarity with animal lippases, particularly phospholipase B.

cc in conjunction with human thyroid and brain cDNAs. The NHL gene is

in conjunction with human thyroid and brain cDNAs. The NHL gene is

cc in conjunction with human thyroid and brain cDNAs. The NHL gene is

co the open reading frame (ORF), resulting in an Ala/Val substitution at

cc of the open reading frame (ORF), resulting in an Ala/Val substitution at

cc treating disorders such as inflammatory or proliferative disease,

cr in screening for compounds useful in the treatment of mental, biological

cc infectious disease, clotting disorders, and cancer. They can also be used

in screening for compounds useful in the treatment of mental, biological

cc medical disorders, as diagnostic reagents, in clinical trial

cc medical disorders, and mutriceutical applications. NHL

monitoring and in cosmetic and mutriceutical applications of disease-

cc cucleotides can additionally be used in the detection of disease-

cc cucleotides can additionally be used in the detection of disease-

cc recombinant expression of NHL, to generate transgenic animals, in gene

cr charapy, and as part of ribozyme and/or triple helix sequences useful in

cc therapy, and as part of ribozyme and/or triple helix sequence represents

cc cDNA encoding the Ala 1318 variant of NHL
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re structurally related to
useful for drug screening,
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Pred. No. 2e-312;
0; Mismatches 0; Indels 190;
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  Polynucleotides encoding human lipases that are structi
animal lipases, particularly phospholipase B, useful fi
diagnosis and in gene therapy of biological disorders.
                                                                                      English
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Matches 1582;
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The invention relates to a novel human lipase (NHL; ABB09555, ABB09556)
and to nucleic acids encoding it (ABQ77623, ABQ77624). The NHL has
extructural similarity with animal lipases, particularly phospholipase B.
Polymucleotides encoding NHL were obtained using human genomic sequences
in conjunction with human thyroid and brain cDNAs. The NHL gene is
coated on chromosome 2, and contains a C/T polymorphism at position 3953
of the open reading frame (ORF), resulting in an Ala/Val substitution at
position 1318 in the protein. NHL nucleotides and proteins are useful for
treating disorders such as inflammatory or proliferative disease,
infectious disease, clotting disorders, and cancer. They can also be used
in screening for compounds useful in the treatment of mental, biological
or medical disorders, as diagnostic reagents, in clinical trial
continuing and in cosmetic and nutriceutical applications. NHL
conitoring and additionally be used in the detection of disease.
cuclectides can additionally be used in the detection of disease.
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/*tag= m
/product= "Human lipase NHL"
replace(3953, C)
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//note= "Single nucleotide polymorphism (SNP); leads to a
Val to Ala substitution at position 1318 of the protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; lipase; chromosome 2; phospholipase B homologue; thyroid; brain; inflammatory disease; proliferative disease; infectious disease; clotting disorder; cancer; drug screening; mental disorder; NHL; diagnostic reagent; clinical trial monitoring; cosmetic; nutriceutical; mutation detection; gene expression analysis; transgenic animal; nootropic; cytostatic; antiinflammatory; single nucleotide polymorphism; SNP; gene therapy; gene; ss.
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                                                                                                             CTCCAATGAGCCTGCGCACTGTGGCCCTCTAG
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recombinant expression of NHL, to generate transgenic animals, in gene therapy, and as part of ribozyme and/or triple helix sequences useful in the modulation of NHL gene expression. The present sequence represents cDNA encoding the Val 1318 variant of NHL. Note: The present sequence is not shown in the specification, but was derived from the the information given on page 18 and the Ala 1318 NHL-encoding cDNA (ABQ77623) given in the sequence listing
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74.1%; Score 1360.4; DB 6; Length 4377;
Best Local Similarity 89.2%; Pred. No. 4.8e-312;
Matches 1581; Conservative 0; Mismatches 1; Indels 190;
                                                                                                                                                                                                         Sequence 4377 BP; 1085 A; 1216 C; 1155 G; 921 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCAGGTGTTCCTGGGAAACCCAGACAAGTGCCCAGTGCAGCAGGCCA-
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chronic obstructive pulmonary disease; cerebrovaccular disease; dementia; Alzheimer's disease; Parkinson's disease; certicobasal degeneration; motor neuron disease; Parkinson's disease; certicobasal degeneration; schizophrenia; korsakoff's psychosis; pain; epilepsy; multiple sclerosis; sciatica; stroke; age associated memory impairment; allergy; asthma; allergic rhinitis; hay fever; atopic dermatitis; cardiovascular disease; anaphylaxis; inflammation; acute respiratory distress syndrome; diabetes; chronic obstructive pulmonary disease; emphysema; observit; anorexia; type-II diabetes; hyperlipidaemia; gall bladder disease; osteoarthritis; gout; sleep apnosa; respiratory problem; polycystic ovarian syndrome; thrombolytic disease; reduced fertility; pregnancy; stress incontinence; hirsutism; menstrual irregularity; depression; enzyme; gene; ss. ww human phospholipase-like enzyme polypeptide useful for screening gents, and in the treatment of cancer, inflammation, diabetes, obesity, central nervous system disorder, or a cardiovascular disorder. cardiovascular disorder; central nervous system disorder; brain injury ct= "Human phospholipase-like enzyme" "CDS does not include start and stop codon" Location/Qualifiers Claim 19; Fig 1; 144pp; English. 09-OCT-2001; 2001WO-EP011641 10-OCT-2000; 2000US-0238445P. 26-DEC-2000; 2000US-0257293P. ď product= .3648 partial, WPI; 2002-426287/45. P-PSDB; AAE22860 (FARB) BAYER AG WO200231161-A2 sapiens 18-APR-2002 zhu z; Ношо

The present invention relates to novel human phospholipase-like enzymes and polymucleotides encoding such proteins. Sequences of the invention are useful for producing a medicament for modulating the activity of phospholipase in a disease such as cancer, inflammation, cardiovascular bhospholipase in a disease such as cancer, inflammation, cardiovascular diseases, chronic obstructive pulmonary disease, certical a disease, dementia (Alzheimer's disease), Parkinson's disease, corticobasal degeneration, motor neuron disease, Pick's disease, Corticobasal degeneration, associated with CNS (e.g. epilepsy, failed back surgery syndrome, castica), multiple sclerosis, stroke, age associated memory impairment, allergic disease including asthma, allergic rhinitis (hay fever), atopic dermatitis, anaphylaxis and inflammation, cardiovascular disease, chronic obstructive pulmonary disease, acute respiratory distress syndrome, gout, cartery disease, hyperlipidaemia, appetension, type-II diabetes, coronary artery disease, hyperlipidaemia, agal bladder disease, prostate, colon cancer), thrombolytic disease, reduced fartility, polycystic ovarian syndrome, complications of pregnancy, menstrual irregularity, human the present sequence is numan phospholipase like enzyme encoding cDNA

Score 1337.2; DB 6; Length 3648; Pred. No. 1.4e-306; Seguence 3648 BP; 899 A; 1032 C; 947 G; 770 T; 0 U; 0 Other; 72.9%; 88.8%; Query Match Best Local Similarity

2008 2428 2308 2608 2728 2788 ë GGGTCAACGACTTGTGTCATTACTGTGAAATCCGGAGGCCCACTTGGCCACGGAATATG 2968 482 CAGCGGAAGGGGCCAGAGCTAGGGACATGCCAGCCCAGGCCTGGGACCTGGTAGAGCGAA 2848 TGAAAAACAGCCCCGACATCAACCTGGAGAAGACTGGAAGCTGGTCACACTCTTCATTG 2908 273 362 422 542 602 662 722 782 842 902 9 2249 GGCTCCCAGATACGTCCTTCTTTGCCCCAGACTGCATCCACCCAAATCAGAAATTCCACT CCCTGGACCTGAGAGCCGAGTCCCCATCACCTCGTCCCACTCAGAATGAGCCCTTCCTGA 843 GGGTCAACGACTTGTGTCATTACTGTGAGAATCCGGAGGCCCACTTGGCCACGGAATATG CTGCAGCCAACTTTGTTCACCATCTCCGCAATGCCTTGGACGTCCTGCATAGAG----------addrececadadrecrearearecrearearerrecrearecreare 2069 ACTGCGTTCTGACCCTGCGGGAGAACTCCCAAGAGCTAGCCAGGCTGGAGGCCTTCAGCC ------GAGCAGCATGCGCGAGCTGGTGGGGTCAGGCCGCTATGACACGCAGGAGG 2129 GAGCCTÁCCGGAGCAGCATGCGCGAGCTGGTGGGGTCAGGCCGCTATGACACGCAGGAGG GAGCTCGACCAAACAACTCCAGTGACCTACCCACATCTTGGAGGGGACTCTTGGAGG TIGGAGGGGATGGGAACTIGGAGACTCACACACACTGCCCAACATTCTGAAGAAGTTCA ACCCTTACCTCCTTGGCTTCTCTACCAGCACCTGGGAGGGGGACAGCAGGACTAAATGTGG 219 ACTICTCTGTGGTGCTGCAGCCCTTCTTCCAGAACATCCAGCTCCCTGTCCTGGC----GTGACTTCCTGTGTACAGAGTGGAAGGCTTCCAATAGTGTTCCAACCTCTGTCCACCAGC TCCGACCAGCAGACATCAAAGTGGTGGCCGCCCTGGGTGACTCTCTGTGACTACAGCAGTGG TCCGACCAGCAGACATCAAAGTGGCCGCCCTGGGTGACTCTCTGACTGTGAGTATGG ACCCTTACCTCCTTGGCTTCTCTTCTCTCTGGCAGGGGGGCACAGCAGGACTAAATGTGG TCCCTTAGGTGCCCAGAGTCCTGGTCAACCTCGTGGACTTCCTGAACCCCACTATCATGC CCCTGGACCTGAGAGCAGAGATGCCCATCACCTGTCCCACTCAGAATGAGCCCCTTCCTGA GAGCTCGACCAAACAACTCCAGTGACCTACCCACATCTTGGAGGGGACTCTCTTGGAGCA TTGGAGGGGATGGGAACTTGGAGACTCACACACTGCCCAACATTCTGAAGAAGTTCA CAGCGGAAGGGGCCAGAGCTAGGGACATGCCAGGCCCAGGCCTGGGACCTGGTAGAGCGAA Gaps Indels 190; 121 GGCAGGTGTTCCTGGGAAACCCAGACAAGTGCCCAGTGCAGCAGGCCA . 8 Mismatches .. Matches 1562; Conservative ----------2189 2369 2549 1901 1955 2009 169 169 274 303 363 2429 423 2489 483 543 2609 5669 663 2729 2789 783 2849 2909 603 723 g 셤 용 셤 a ઠે 셤 g 셤 셤 셤 셤 셤 8 ઠે ठे ò ઠે õ ò 8 ઠે ò g 8 a 8 g ò 셤 ò 용 ð 유 ਨੇ

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Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;
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Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;
Lepley DW, Rieger DK;
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16-MAY-2001; 2001US-0291040P.
16-MAY-2001; 2001US-029140P.
13-MAY-2001; 2001US-0294489P.
11-MAY-2001; 2001US-0294899P.
13-MAY-2001; 2001US-0294899P.
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19-JUN-2001; 2001US-0299310P.
10-JUN-2001; 2001US-0299310P.
11-JUL-2001; 2001US-03993P.
11-MAY-2001; 2001US-03993P.
11-MAY-2001; 2001US-03993P.
11-MAY-2001; 2001US-03993P.
11-SEP-2001; 2001US-0318462P.
12-SEP-2001; 2001US-0318462P.
12-SEP-2001; 2001US-03189P.
13-CT-2001; 2001US-0339380P.
13-CT-2001; 2001US-0339380P.
08-MAR-2001; 2001US-0274194P.
08-MAR-2001; 2001US-0274281P.
08-MAR-2001; 2001US-0274281P.
09-MAR-2001; 2001US-027432P.
09-MAR-2001; 2001US-027432P.
13-MAR-2001; 2001US-0275578P.
13-MAR-2001; 2001US-0275579P.
13-MAR-2001; 2001US-027560P.
14-MAR-2001; 2001US-02760P.
15-MAR-2001; 2001US-027699P.
20-MAR-2001; 2001US-027732P.
21-MAR-2001; 2001US-027732P.
22-MAR-2001; 2001US-027732P.
23-MAR-2001; 2001US-027732P.
23-MAR-2001; 2001US-027733P.
27-MAR-2001; 2001US-027733P.
27-MAR-2001; 2001US-027733P.
27-MAR-2001; 2001US-027733P.
27-MAR-2001; 2001US-027899P.
27-MAR-2001; 2001US-027939P.
27-MAR-2001; 2001US-027939P.
27-MAR-2001; 2001US-027939P.
27-MAR-2001; 2001US-027934P.
20-MAR-2001; 2001US-0280900P.
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20-MAR-2001; 2001US-0280900P.
20-APR-2001; 2001US-0280900P.
20-APR-2001; 2001US-028096P.
20-APR-2001; 2001US-028096P.
20-MAY-2001; 2001US-028096P.
20-MAY-2001; 2001US-028096P.
20-MAY-2001; 2001US-028096P.
20-MAY-2001; 2001US-028052P.
20-MAY-2001; 2001US-028096P.
20-MAY-2001; 2001US-028096P.
20-MAY-2001; 2001US-028096P.
20-MAY-2001; 2001US-028019P.
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20010S-0333184P
20010S-0333184P
20010S-0332094P
20010S-033792P
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20010S-0331892P
20010S-033185P
20010S-033185P
20020S-0345P
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      CTGAAGAGCCCCCGAGGTGCTCTACTGGGCTGTCCCAGTGGCAGCGGAGTCGGCCTTG 1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer; hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine; human; gene; 88.
                                                                                                                         963 ACGTGGTGGAGGTCATGGAGCTGGCTACCTGTACCAGGCCAAGGCGGAAATGTGCCA 1022
1029 ACGTGGTGGAGGTCATGGAGCTGGTAGCCTGTACCAGGGCCAAGGCGGGAAATGTGCCA 3088
                                                                                                                                                                                                                                                                                 TTCAGCACATCCAACAAGCCCTGGACATCCTCTGTGAGGAGCTCCCAAGGGCTTTCGTCA
                                     CTCCAATGAGCCTGCGCACT 3648
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treating NOVX polypeptides and polynucleotides, useful for preventing or trea a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma.

P-PSDB; ABU65081

Claim 13; Page 167-168; 1103pp; English

cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABX9708-ABX97185 are CDNA fragments amplified and isolated by the PCR primers and probes represented in ABX13460-ABX13462 and ABX97186-ABX97593. ABX97108-ABX97185 encode the NOVX proteins described in This invention describes novel human NOVX polypeptides which have ABU65041-ABU65218

Sequence 4268 BP; 1039 A; 1209 C; 1119 G; 901 T; 0 U; 0 Other;

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2569 7; -----AGGTGCCCAGAGTCCTGGTCAACCTCGTGGACTTCCTGAACCCCACTATCATGC 2623 ACTICICION DE LA CARGO DEL CARGO DE LA CARGO DEL CARGO DE LA CARGO DEL CARGO DEL CARGO DE LA CARGO DEL CARGO DE LA CARGO DEL LA CARGO 2684 ACTGCGTTCTGACCCTGCGGGAGAACTCCCAAGAGCTAGCCAGGCTGGAGGCCTTCAGCC 2743 2744 GAGCCTACCAGAGCAGCATGCGCGAGCTGGGGGTCAGGCCGCTATGACACGCAGGAGG 2803 2924 CCCAGCTGGCCAGAGCCCTTTGGACCAATATGCTTGAACCACTTGGAAGCAAACAGAGA 2983 2864 GGCTCCCAGATACGTCCTTCTTTGCCCCAGACTGCATCCACACAAATCAGAAATTCCACT 2923 61 TCCCTTAGGTGCCCAGAGTCCTGGTCAACCTCGTGGACTTCCTGAACCCCACTATCATGC 120 165 -----CCAGAGCAGCATGCGCGAGCTGGTGGGTCAGGCCGCTATGACACGCAGGAGG 218 -----GCGCTTGAACCACTTGGAAGCAAACAGAGA 302 GTGACTTCCTGTGTACAGAGTGGAAGGCTTCCAATAGTGTTCCAACCTCTGTCCACCAGC 482 | TCCGACCAGCAGACATCAAAGTGGTGGCCGCCCTGGGTGACTCTCTGACTACAGCAGTGG 542 ACTICICIGIGGIGCIGCAGCCCTTCTTCCAGAACATCCAGCTCCCTGTCCTG----- 271 CCCTGGACCTGAGAGCAGAGATGCCCATCACCTGTCCCACTCAGAATGAGCCCTTCCTGA 362 1 CTGCAGCCAACTTTGTTGACCATCTCCGCAATGCCTTGGACGTCCTGCATAGAGAGCTTT 60 CTGCAGCCAACTTTGTTCACCATCTCCGCAATGCCTTGGACGTCCTGGATAGAG-----Gaps Score 1231.8; DB 6; Length 4268; Pred. No. 1.5e-281; 0; Mismatches 37; Indels 211; GGCAGGTGTTCCTGGGAAACCCAGACAAGTGCCCAGTGCAGCAGG 67.1**%**; 86.1**%**; Best Local SIMILALLY COMMETCHES 1535; Conservative ------2516 2570 2624 2804 121 166 166 2984 3044 3104 483 Query Match 219 272 272 303 363 423

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Db	3164	TCCGACCAGCAGACATCAAAGTGGTGGCCGCCCTGGGTGACTCTCTGACTACAGCAGTGG 3223
č	543	GAGCTCGACCAAACAACTCCAGTGACCTACCCACATCTTGGAGGGACTCTCTTGGAGCA 602
qq	3224	GAGCTCGACCAACAACTCCCAGTGACCTACCCACATCTTGGAGGGGACTCTTGGAGCA 3283
δ,	603	TIGGAGGGATGGGAACTIGGAGACTCACACCACACTGCCCAACATTCTGAAGAAGTICA 662
qq	3284	THGABGGGGATGGGGAACTTGGAGACTCACCACACTGCCCAGTATTCTGAAGAAGTTCA 3343
ò	663	ACCTTACTCCTTGGCTTCTCTACCAGCACCTGGGAGGGGACAGGAGGACTAAATGTGG 722
qq	3344	Acceriacercentesenteretaceageaceroseageacadeacadearaanteros 3403
ò	723	CAGCGGAAGGGGCAAGACTAGGACATGCCAGCCCAGGCCTGGGACCTGGTAGAGC 779
qq	3404	cadeceaadedeceadadetragadedaceaceceadeceadeceadeceadeceadecea
ò	780	GAATGAAAAACAGCCCGGACATCAACTGGAAGACTGGAAGCTGGTCACACTCTTCA 839
qq	3464	GAATGAAAAACAGCCCCATACACTTTCAGGAAGACTGGAAGATAATAACCCTGTTTA 3520
ò	840	TIGGGGTCAACGACITGIGTCAITAGTGTGAGAATCCGGAGGCCCACITGGCCACGGAAT 899
qq	3521	ragacagcaargacricrgrgarricrgcaargarcrggraggrgaar 3568
ò	900	
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DP DP	3629	
ò	1020	CCATGCTGGCAGCTCAGAACAACTGCACTTGCCTCAGACACTCGCAAAGCTCCCTGGAGA 1079
qq	3689	
λΌ	1080	AGGAAGAACTGAAGAAAGTGAACTGGAACCTCCAGCATGGCATCTCCAGTTTCTCCTACT 1139
qa	3749	
ò	1140	GGCACCAATACACACAGCGTGAGGACTTTGCGGTTGTGGTGCAGCCTTTCTTCCAAAAA 1199
qa	3809	GGCACCAATACACACAGCGTGAGGACTTTGCGGTTGTGGGTGCAGCCTTTCTTCCAAAACA 3868
δy	1200	
qq	3869	
ò	1260	
qq	3926	
ò	1320	AACCAGTGGGCCGCAAGACTACCTCCAACAACTTCACCCACAGCCGAGCCAAACTCAAGT 1379
qq	3986	
ò	1380	
qq	4046	
ò	1440	AGGCTGAAGAAGCCCCCGAGGTGCTCTACTGGGCTGTCCCAGTGGCAGCGGGAGTCGGCC 1499
Dp	4106	
λŏ	1500	Tigióciqececateatecaecaecaecaeses 1559
qq	4166	
λ̈	1560	AICCICCAATGAGCCTGCGCACTGTGGCCCTCTAGGCCCGGGG 1602
qq	4226	426

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2684 ACTGCGTTCTGACCCTGCGGGAGAGATCCCCAAGAGCTAGCCAGGCTGGAGGCCTTCAGCC 2743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to 566 new isolated human polypeptides and their encoding genes, sequences that are at least 95% identical to these or sequences comprising one or more conservative substitutions in these. The polypeptide of particular conservative substitutions in these. The polypeptide and antibodies against the polypeptides are useful in diagnosing, treating or preventing NoVX-associated disorders, e.g. cardiomyopathy, atherosolerosis, hypertension, cancer, obesity, diabetes, ADS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, parkinson's disease, asthma, or fertility disorders. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The example of the nucleic acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                  Burgess CE, Casman SJ, Catterton E, Dhanabal W, Edinger SF, Burgess CE, Casman SJ, Catterton E, Dhanabal W, Edinger SF, Bilerman K, Ettenberg S, Gangolli EA, Gardacha VL, Gorman L, Grose WM, Guther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R; Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR; Maclachlan T, Malyanker UM, Moquener K, Mezick AJ, Miller CE; Millet I, Padigaru M, Payman JA, Qian X, Rastelli L; Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G; Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ; Wolenc AR, Zhong M, Zhong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atheroscierosis or diabetes, in chromosome mapping, tissue typing or in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4268 BP; 1039 A; 1209 C; 1119 G; 901 T; 0 U; 0 Other;
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Dhanabal M, Edinger SR,
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15-AUG-2002; 2002US-0403617P.
15-AUG-2002; 2002US-0403732P.
26-AUG-2002; 2002US-0410085P.
13-SEP-2002; 2002US-0410085P.
13-SEP-2002; 2002US-041055P.
23-GCT-2002; 2002US-041295F.
23-GCT-2002; 2002US-041295F.
23-GCT-2002; 2002US-0420718P.
24-GCT-2002; 2002US-0420718P.
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24-GCT-2002; 2002US-0420718P.
24-GCT-2002; 2002US-042075P.
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P-PSDB; ADH42427.
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                                                                                                                                                                                                                                                                             ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; antiinfertility; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease; Parkinson's disease; asthma; fertility disorder; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; vaccine.
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2002US-0387869P-
2002US-038794P-
2002US-038794P-
2002US-0388022P-
2002US-0388479P-
2002US-0388479P-
2002US-0389120P-
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13-AUG-2002; 2002US-0403458P.
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2002US-0386355P.
2002US-0386357P.
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26-MAR-2001; 2001US-0278894P.
27-MAR-2001; 2001US-0278999P.
28-MAR-2001; 2001US-0279936P.
30-MAR-2001; 2001US-0279944P.
30-MAR-2001; 2001US-0279995P.
30-MAR-2001; 2001US-028023P.
02-APR-2001; 2001US-0280802P.
02-APR-2001; 2001US-0280900P.
04-APR-2001; 2001US-0281444P.
13-APR-2001; 2001US-0281444P.
13-APR-2001; 2001US-0281444P.
13-APR-2001; 2001US-0281444P.
13-APR-2001; 2001US-0281444P.
13-APR-2001; 2001US-0281424P.
13-MAY-2001; 2001US-0288528P.
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GANGOLLI E A.
VERNET C A M.
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GERLACH V.
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SPADERNA S K.
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ZERHUSEN B D.
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MILLER C E.
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ZHONG H.
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PENA C E A.
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10-SEP-2001;
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The invention relates to an isolated polypeptide (designated NOVX, or CC NOV1-NOV127) comprising a sequence selected from 178 fully defined amino acid sequences (and their mature forms, variants and fragments). Also acid sequences (and their mature forms, variants and fragments). Also caid sequences (and their mature forms, variants and fragments). Also comprising the nucleic acid molecule encoding NOVX, a vector included are an isolated nucleic acid determining the presence or the nucleic acid determining the presence of or molecule in a sample, methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian of the above polypeptide, a method for identifying an agent that binds to the above collappetide, a method for identifying a potential therapeutic agent for polypeptide, a method of activity or of latency or predisposition to screening for a modulator of activity or of latency or predisposition to screening for a modulator of activity or of latency or predisposition and method of a pathology associated with the polypeptide and a method for modulating a pathology associated with the polypeptide and a method for modulator of activity or of latency or predisposition and method of a pathology associated with the polypeptide and a method for modulator of activity or of latency or predisposition and method of a pathology associated with the polypeptide and a method for modulator of activity or of activity or of the polypeptide cited above. The composition and method disposes, namenced disposesses and namenced disposesses and namenced dis New NOVX polypeptides and nucleic acid molecules useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or Ë Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li I Gusev VY, Ji W, Gorman L, Miller CE, Kekuda R; Gangolli EA, Vernet CAM, Guo XS, Tchernev VT; Casman SJ, Malaymkar UW, Gerlach V, Liu Y; Spaderna SK, Catterton E, Leite MW, Zhong H; Lepley DM, Rieger DK, Burgess CE; Sequence 4268 BP; 1039 A; 1214 C; 1114 G; 901 T; 0 U; 0 Other; Claim 17; SEQ ID NO 81; 786pp; English. WPI; 2004-225693/21. P-PSDB; ADN61813. RIEGER D K. BURGESS C E. pharmacogenomics. Patturajan M, (Fernandes ER, (Anderson DW, Si Alsobrook JP, Padigaru M, Zerhusen BD, Query Match (RIEG/) F (BURG/) I

67.0%; Score 1230.2; DB 12; Length 4268; 86.0%; Pred. No. 3.6e-281; tive 0; Mismatches 38; Indels 211; Gaps Best Local Similarity 86.0 Matches 1534; Conservative

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2684 ACTGCGTTCTGACCCTGCGGGAGAACTCCCAAGAGCTAGCCAGGCTGGAGGCCTTCAGCC 2743 2570 -----AGGTGCCCAGAGTCCTGGTCACCTCGTGGACCTCCTGAACCCCACTATCATGC 2623 165 61 TCCCTTAGGTGCCCAGAGTCCTGGTCAACCTCGTGGACCTCCTGAACCCCCACTATCATGC 120 1 cręchacchactrigitanccarcrececharecerrecarcerecaragadaerrr 60 -----ccagagcagcargcagcragcragagcragagccagcrargacacacagaag 121 GGCAGGTGTTCCTGGGAAAGCCAGACAAGTGCCCAGTGCAGCAGCAGG 166 ------, g 셤 Š Š g

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0y 1260 TTCACTTCTCAGACCGGGGGATGCCGAGATGGCATCGGACTCTGGAACAACATGCTGG 1319 0y 1320 TTCACTTCTCAGACCGGGGGATGCCGAGATTGGCACTCTGGAACACATGCTGG 1385 0y 1320 AACCAGTGGGCCGAAGATTCACCTCCACAGCTCTGGAACTCAAGT 1379 0y 1386 AACCAGTGGGCCGAAGATTCACCTCCACAGCCGAGCCAAACTCAAGT 1405 0y 1380 GCCCTTCTCAGAGCTACCTCCACACACTCCACCAGCCGAGCCAAACTCAAGT 1405 0y 1380 GCCCTTCTCAGAGACTACCTCAACAACTCACCCAGGCCGAACTCAAGT 1405 0y 1410 GCCCTTCTCTGTGAGTCCTTACCTCTACCCTGGGAACAGCCGATTGCTCCCAGACC 1105 0y 1410 AGGCTGAAGAAGCCCCCGAGGGTGCTCTACTGGGCTGTCCCAGTGGCAGGGGAGTCGGCC 1405 0y 1500 TTGTGGTGGGATCATCGGGACTGTCCCAGTGCCCGGGGGAGTCGGCCGGAGGGAG	Search completed: March 26, 2005, 14:31:15 Job time : 982.6 secs	Y!
2804 ACTTCTCTGTGGTGCTGCAGCCTTCTCCAGAACATCCAGCTCCTGTCCTGCAGGATG 2863 272	GAGCTCGACCAACAACAACTCCAGTGACCTACCCACATCTTGGAGGGGACTCTTTTGGAGCGCAACAACAACAACTCCAGTGACCTACCCCACATCTTGGAGGGGACTCTTTTGGAGGGGACTCTTTTGGAGGGGACTCTTTTGGAGGGGACTCTTTTTGAGGGGGATGCTACTTTTGAGGGGACTCTCTTTTGAGGGGATGCGAACTTCTTTTTTTT	1080 ACCACACACTGAACTGAACCTCCACCAGGATCCCCAGTTCCCCTACT 1139 ACCAAGAACTGAACGTCCCCAGTTCCCTACT 1139 ACCAAGAACTGAACGTGAACCTCCCAGGTTCCCTACT 1139 ACCAAGAACTGAACGAACCTGCAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTTCTCCCAAAACA 1199 ACCAACAAACAAACAAACAAACAAACAAACAAACAAA
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sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 179, App Sequence 179, App Sequence 14123, A Sequence 14123, A Sequence 1103, A Sequence 17, Appli Sequence 27, Appli Sequence 11, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli

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TCCCTTAGGTGCCCAGAGTCCTGGTCAACCTCGTGGACTTCCTGAACCCCACTATCATGC 120
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Patent No. 6822072

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Huma:
FILE REFERENCE: GENSET. 025CP1
CURRENT APPLICATION NUMBER: US/09/471,276
CURRENT APPLICATION NUMBER: US/09/471,276
CURRENT APPLICATION NUMBER: 09/057,719
EARLIER FILING DATE: 1998-12-21
EARLIER FILING DATE: 1998-04-28
EARLIER FILING DATE: 1998-04-28
EARLIER FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: PETENT OF NUMBER: PCT/IB99/00712
EARLIER FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: PATENT OF NUMBER: PCT/IB99/00712
EARLIER FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: PATENT OF NUMBER: PCT/IB99/00712
EARLIER FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: PATENT OF NUMBER: PCT/IB99/00712
EARLIER FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: PATENT OF NUMBER: PCT/IB99/00712
EARLIER FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: PATENT OF NUMBER: PCT/IB99/00712
EARLIER FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 1622
US-09-621-976-15353
US-07-945-288-9
US-08-462-831-9
US-08-461-809-9
US-08-46-441-9
PCT-US93-08518-9
US-09-449-016-14123
US-09-949-016-14383
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US-09-949-016-14383
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US-09-829-481-3
US-09-829-481-3
US-09-829-481-3
US-09-829-481-3
US-09-844-469-5
US-09-388-4138-5
US-09-388-4138-5
US-09-346-469-5
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OTHER INFORMATION: SEG LWCCSPSSRTSSS/LS
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NAME/KEY: sig peptide
LOAD: 276..335
OTHER INFORMATION: Von Heijne matrix
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OTHER INFORMATION: Oligonucleotide
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Best Local Similarity 69.9
Matches 251; Conservative
                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
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Sequence 27, Appl
Sequence 10, Appl
Sequence 5, Appli
Sequence 12892, A
Sequence 12892, A
Sequence 161396,
Patent No. 5498694
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Sequence 10543, A
Sequence 78, Appl
Sequence 1, Appli
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16264, A
9851, Ap
11902, A
927, App
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Sequence 12725, A
Sequence 28539, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17854, A
24, Appl
24, Appl
14178, A
41, Appl
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                                                                                                                                                                                                      March 26, 2005, 13:16:45 ; Search time 322.751 Seconds
    (without alignments)
    9303.061 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                      Description
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*
(cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-800-729-11

US-09-920-729-11

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US-09-949-016-161396

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US-09-949-016-161396

US-09-311-021-107

US-09-311-021-107

US-09-270-767-11902

US-09-270-767-11902

US-09-21-976-937

US-09-210-976-937

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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Minimum DB Maximum DB

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Searched:

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                                      APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids us (186.094
TITLE REPREBRICE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28539
LENGTH: 323
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2.7%; Score 49.6; DB 4; 1

Best Local Similarity 80.6%; Pred. No. 0.014;

Matches 58; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
TITLE OF INVENTION: 32 Human secreted proteins
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT PILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 62.2; DB 4;
Pred. No. 1.1e-06;
0; Mismatches 68;
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 35, Application US/09800729
; Patent No. 6605592
                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Drosophila melanogaster US-09-270-767-28539
                                                                                                                                                                                                                                                                                                                                                                                                                                      3.4%;
Best Local Similarity 60.2%;
Matches 103; Conservative (
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LOCATION: (6035)
OTHER INFORMATION:
Patent No. 6703491
GENERAL INFORMATION:
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LOCATION: (603
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                                                                                                                                                                                                                                                                                                         178
                                                                                                                                                                                                                                                172 ACTGCGTTCTGACCCTGCGGGAGAACTCCCAAGAGCTAGCCAGGCTGGRGGCCTTCAGCC 231
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                                                                                                      278
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US-09-270-767-12725
US-09-270-767-12725, Application US/09270767
Sequence 12725, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
CURRENT APPLICATION NUMBER: 1326-034
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12725
LENGTH: 645
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                                                                   GGCAGGTGTTCCTGGGAAACCCAGACAAGTGCCCAGTGCAGCAGCCCAGAGCAGCATG--
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Best Local Similarity 56.2%; Pred. No. 1.2e-18;
Matches 227; Conservative 0; Mismatches 168;
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US-09-270-767-28539
; Sequence 28539, Application US/09270767
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; ORGANISM: Drosophila melanogaster
US-09-270-767-12725
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1094 AAAAAAAAAAAAAA 1110
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ORGANISM: Homo sapiens
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Matches 53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.7%; Score 49.4; DB 4; Length 193; Best Local Similarity 78.7%; Pred. No. 0.0023; Matches 59; Conservative 0; Mismatches 16; Indels (
                                                                                                                                                                    APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTB and Encoded Human Proteins.
FILE REPERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 10543
LENGTH: 193
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TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
FRIOR PELING DATE: 2000-09-22
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
                                                                                                   ; Sequence 10543, Application US/09621976; Patent No. 6639063; GENERAL INCORMATION: APPLICANT: Dumas Milne Edwards, J.B.
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Patent No. 6605592
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
i_LOCATION: 36..37
CTHER INFORMATION: n=a, g, c or t
US-09-621-976-10543
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5975 AAAAAAAAAA 5986
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; ORGANISM: Homo sapiens
US-09-800-729-78
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59; Conserv
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APPLICANT: Batra. Surinder K.
APPLICANT: Batra. Surinder K.
APPLICANT: Batra. Michael A.
APPLICANT: University of Nebraaka Board of Regents
TITLE OF INVENTION: No. 66801964 Gene That is Amplified and
TITLE OF INVENTION: Overexpressed in Cancer and Methods of Use Thereof
FILE REFERENCE: UNMCG3121
CURRENT APPLICATION NUMBER: US/09/647,143
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: E07/US99/06633
PRIOR APPLICATION NUMBER: 60/079,649
PRIOR PILING DATE: 1999-03-27
PRIOR PILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PSECSO for Windows Version 3.0
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86.9%; Pred. No. 0.018;
tive 0; Mismatches 8; Indels 0.
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Patent No. 6605592;
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins;
FILE REPERENCE: PZ044P1;
CURRENT APPLICATION NUMBER: US/09/800,729;
CURRENT FILING DATE: 2001-03-08;
PRIOR PILING DATE: 2000-09-22;
PRIOR PILING DATE: 1999-09-24;
PRIOR FILING DATE: 1999-09-24;
NUMBER OF SEQ ID NOS: 217;
SOFTWARE: PATENTIN VEY: 2.0
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Sequence 1, Application US/09647143
Patent No. 6680196
GENERAL INPORMATION:
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Matches 59; Conservative
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Query Match 2.6%;
Best Local Similarity 72.6%;
Matches 61; Conservative
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Felyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Mehrman, Tom
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John Tillinghast
Drmanac, Radoje
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; ORGANISM: Triticum aestivum
US-09-370-473-5
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Wang, Jian-Rui
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Wang, Zhiwei
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Ma, Yunqing
                                               1834 AA 1835
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; Patent No. 653701
; TITLE OF INVENTION: ANTIBENSE MODULATION OF SAP-1 EXPRESSION TITLE OF INVENTION: ANTIBENSE MODULATION OF SAP-1 EXPRESSION FILE REFERENCE: RTS-0267
; CURRENT APPLICATION NUMBER: US/09/920,759
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 91
; LENGTH: 1976
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85.5%; Pred. No. 0.026; tive 0; Mismatches 9; Indels 0.
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                                                                                                                  GENERAL INFORMATION:
APPLICANT: Ni et al.
APPLICANT: Ni et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT APPLICATION NUMBER: S010-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-09-24
NUMBER OF SEQ ID NOS: 217
SEQ ID NO 27
LENGTH: 2355
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2.6%; Score 48.2; DB
Best Local Similarity 76.6%; Pred. No. 0.02;
Matches 59; Conservative 0; Mismatches
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CTHER INFORMATION: n equals a,t,g, or C
US-09-800-729-27
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: SITE
LOCATION: (22)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: SITE
                                                                                 ; Sequence 27, Application US/09800729
; Patent No. 6605592
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2282 AAAAAAAAAAAAAA 2298
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Query Match
Best Local Similarity 85.5
Matches 53; Conservative
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LOCATION: (150) ... (1367)
US-09-920-759-10
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LENGTH: 688
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Sequence 161396, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-10-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

WINDBER OF SEQ ID NOS: 207012
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86.7%; Pred. No. 0.053;
tive 0; Mismatches 8; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12892, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Unmas Milne Edwards, J.B.
APPLICANT: JODERT, S.
APPLICANT: Glordano, J.Y.
TITLE OF INFORTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 12892
LENGTH: 130
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1.105
SOFTWARE: Pt_f_genes Version 1.0
SEQ ID NO 861
LENGTH: 4494
                                                                                                                                                                                                                                                                    Best Local Similarity 86.7
Matches 52; Conservative
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Matches 56; Conservative
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; LOCATION: (207)..(3002)
US-09-620-312D-861
                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-621-976-12892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5498694; APPLICANT: RUGSLAHTI, ERKKI I.; APPLICANT: RUGSLAHTION: PEPTIDES OF THE CYTOPLASMIC DOMAIN OF
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 161396
LENGTH: 601
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,967
FILING DATE: 10-MAY-1994
PRIOR APPLICATION NUMBER: 973,547
FILING DATE: 09-NOV-1992
APPLICATION NUMBER: 357,824
FILING DATE: 25-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       completed: March 27, 2005, 03:58:53
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                                                                                                       US-09-949-016-161396
                                                             TYPE: DNA
ORGANISM: Human
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Sequence Sequence Sequence

Sequence 3816, Ap Sequence 7744, Ap Sequence 526, App Sequence 68350, A Sequence 9532, Ap Sequence 9131, Ap Sequence 115890, Sequence 115890, Sequence 1677, Ap Sequence 1650, A Sequence 66929, A Sequence 66929, A Sequence 303, Ap Sequence 303, Ap Sequence 1648, Ap Sequence 1650, A Sequence 1648, Ap Sequence 139428, Sequence 71, Appl

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database

Sequence 71, Appl Sequence 71, Appl Sequence 483, App Sequence 71, Appl Sequence 71, Appl Sequence 71, Appl

Sequence 483,

CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: PCT/US02/15688
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: US 60/292,242
PRIOR PILING DATE: 2001-05-18
PRIOR PELING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/293,726
PRIOR APPLICATION NUMBER: US 60/295,346
PRIOR PILING DATE: 2001-06-01

Sequence 11, Appl Sequence 85, Appl Sequence 11, Appl Sequence 81, Appl Sequence 73, Appl Sequence 123, Appl Sequence 1331, Appl Sequence 83, Appl

US-10-478-245-19 US-10-478-245-11 US-10-092-900A-85 US-10-054-691-1 US-10-254-691-1 US-10-254-174-73 US-10-256-115-600 US-10-264-237-323 US-09-764-891-1391 US-10-092-900A-83

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1555.2 1421 1421 1362 1231.8 667.4 667.4 667.4 130.6 210.6

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Sequence 19, App]

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Sequence 4 Sequence Sequence

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                                                                                                                                        Length 4424;
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                                                                                                                                        DB 18;
                                                                                                                                       Score 1649.2; State 1649.2; Similarity 95.1%; Pred. No. 0; 11; Conservative 0; Mismatches
                                                                                                    NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7504684CB1
US-10-478-245-19
          PRIOR APPLICATION NUMBER: US 60/351,262
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/368,799
PRIOR FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO 19
                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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Matches 1731; C
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                                                       GENERALL INFORMATION:

APPLICANT: INFORMATION:

APPLICANT: YUE, Henry; AZIMZAI, Yalda;

APPLICANT: BAUGHN, Mariah R.; BURFORD, Neil;

APPLICANT: BAUGHN, Mariah R.; BURFORD, Neil;

APPLICANT: BEDDY, Debopriya: NGUYEN, Danniel B.;

APPLICANT: TAD, Debopriya: NGUYEN, Danniel B.;

APPLICANT: TAD, Wanigue G.; ARVIZU, Chandra S.;

APPLICANT: GRIFFIN, Jennifer A.; ELLIOTT, Vicki S.;

APPLICANT: GRIFFIN, Jennifer A.; ELLIOTT, Vicki S.;

APPLICANT: LU, Yan; GANDHI, Ameena R.;

APPLICANT: LU, Yan; GANDHI, Ameena R.;

APPLICANT: LU, Yang Aina M.; LEE, Ernestine A.;

APPLICANT: LU, Dyung Aina M.; LEE, Ernestine M.;

APPLICANT: LU, Dyung Aina M.; LEE, Ernestine M.;

APPLICANT: YANG, Juuming; TRIBOULEY, Catherine M.;

APPLICANT: ANG, Juuming; TRIBOULEY, Catherine M.;

APPLICANT: LLPID-ASSOCIATED MOLECULES

TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES

TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES

CURRENT APPLICATION NUMBER: DG 0/292, 242

PRIOR FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: US 60/293, 726

PRIOR APPLICATION NUMBER: US 60/293, 726

PRIOR APPLICATION NUMBER: US 60/303, 404

PRIOR APPLICATION NUMBER: US 60/314, 754

PRIOR APPLICATION NUMBER: US 60/314, 754

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: 2001-06-01

PRIOR PILING DATE: 2002-03-29

PRIOR PILING DATE: 2002-0
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; Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2440624CB1
US-10-478-245-11
Application US/10478245
10. US20040171009A1
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Best Local Similarity 90.2
Matches 1799; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Alsobrook, John P.
APPLICANT: Alsobrook, John P.
APPLICANT: Lepley, Denial R.
APPLICANT: Reger, Daniel R.
APPLICANT: Reger, Daniel R.
APPLICANTON: NUMBER: US0040043382Alel Proteins and Nucleic Acids Encoding Same File Reperrence: 2002-03-07
CURRENT PILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/274,322
PRIOR APPLICATION NUMBER: USSN 60/274,281
PRIOR APPLICATION NUMBER: USSN 60/274,281
PRIOR APPLICATION NUMBER: USSN 60/274,191
PRIOR PILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/279,995
PRIOR APPLICATION NUMBER: USSN 60/279,995
PRIOR APPLICATION NUMBER: USSN 60/294,899
PRIOR APPLICATION NUMBER: USSN 60/294,899
PRIOR PILING DATE: 2001-05-13
PRIOR PILING DATE: 2001-05-13
PRIOR PILING DATE: 2001-05-13
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: USSN 60/294,899
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: USSN 60/294,899
PRIOR PILING DATE: USSN 60/294,899
PRIOR PILING DATE: USSN 60/287,424
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: (16)..(4285)
US-10-092-900A-85
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                                                                                                                                  1683 TTC-AATGCCTGGTGCCATAGGAAGCCCA-GGGGACAGTCACAACTTCTTGGGGGCCTGGG
                                                                                                                                                                                                                        TGGTGGGCATCATCGGGACAGTGGTGGAGGTGCAGGAGGTGGCCGGAGGAAGATC
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                                                 CAGTGGGCCGCAAGACTACCTCCAACAACTTCACCCACAGAGCCAAACTCAAGTGCC
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Sequence 85, Application US/10092900A
Sequence 86, Application US/10092900A
Publication No. US20040043382A1
GENERAL INFORMATION:
APPLICANT: SPYCEK, Kimberly A.
APPLICANT: Shenoy, Sureen G.
APPLICANT: Taupier Jr., Arymond J.
APPLICANT: Pera, Carol E.A.
APPLICANT: Li, Li
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Melales E.
APPLICANT: Miller, Charles E.
APPLICANT: Kekuda, Rameeh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guo, Xiaojia Sasha
Tchernev, Velizar T
Fernandes, Elma R.
Casman, Stacie J.
Malyankar, Uriel M.
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patturajan, Meera
Gangolli, Esha A.
Vernet, Corine A.M.
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APPLICANT:
APPLICANT:
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Anderson, David W. Spaderna, Steven K. Catterton, Elina Leite, Mario W.

--GCGCTTGAACCACTTGGAAGCAAAACAGAGA 302

Db 4013 AACCAGTGGGCCGCAAGACTACCTCCAACAACTCACCCACAGCCGAGCCAAACTCAAGT 4072 Oy 1380 GCCCCTCCTGAGAGCCCTTACCTCTACACCCTGCGGAACAGCCGATTGCTCCCAGACC 4132 O 1400 AGGCTGAAGAGCCCTTACCTCTACACCCGGGAACAGCCGATTGCTCCCAGACC 4132 O 1410 AGGCTGAAGAAGCCCCCGAGGGCTCCTCTCACGGGGAACAGCGGGATTGCTCCCAGACC 4192 O 1500 TTGTGGTGGGCATTCATCGGGTTGCTCCAGTGGCAGGGGAAG 1559 O 1500 TTGTGGTGGGCATTCATCGGGTTGCTTGGGCTGTCCCAGTGGCGGGAGGTGGCCGGAGGGAAG 4252 O 1500 TTGTGGTGGGCATTCATCGGGTTGGTCTGGGCTGTCCCAGTGGCGGGGAAG 4252 O 1500 TTGTGGTGGGCATTCATCGGGTTGGTCTGGGCTGGTGCCCGGGGGGAAG 4252 O 1500 TTGTGGTGGGCATCATCGGGCTTGGTCTGGGCTGGTGGGGGAAG 4252 O 1500 TTGTGGTGGGCATCATCGGCCTTGAGGCTGGGGGGGGGG	RESULT 4 US-10-054-691-1 Sequence 1, Application US/10054691 Sequence 1, Application No. US20020115846A1 Sequence 1, Application No. US20020115846A1 Sequence 1, Application No. US20020115846A1 Sequence 1, APPLICANT: Y. Kuanchuan TAPLICANT: Turner, C. Alexander Jr. TITLE OF INVENTION: No. US20020115846A1e1 Human Lipase and Polymucleotides Encoding til FILE REFERENCE: LEX-0303-USA CURRENT APPLICATION NUMBER: US/10/054,691 CURRENT APPLICATION NUMBER: US 60/264,049 PRIOR PILING DATE: 2001-01-24 NUMBER OF SEQ ID NOS: 2 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 4377 TYPE: DNA CREANISM: homo sapiens US-10-054-691-1	Query Match 74.2%; Score 1362; DB 13; Length 4377; Best Local Similarity 89.3%; Pred. No. 0; Matches 1582; Conservative 0; Mismatches 0; Indels 190; Gaps 3; Qy 1 CTGCAGCCAACTTTGTACACTCTCGCAATGCTTGGACGTCTGCATAGAGGTTT 60 Db 2618 CTGCAGCCAACTTTGTGACCTCTGGAGGTCTGGAGGTCTGGAGGTCTGCAATAGAGGTCTGAACGCTGCAATAGAGGTCTGAACGTCGAATGCTTGGAGGTCTGAACGCTGAATGCTTGAACGCCCAATAGAGGTCTGAACGCCAATAGAGGTCTGAACGCTGAACGCAATGCTGAACGCCAATAGAGGTCTGAACGCCAATAGAGGTCTGAACGCCAATAGAGTCTGAACGCCAATAGAGTCTGAACGCCAACAGACCCAATAGAGTCTGAACGCCAACAGACCCAATAGAGTACTGAACAGTGCCAATAGAACTCCTAAACAGTGCCAATAGAACTCCTAAACAGTGCCAATAGAACTCCTAAACAGTGCCCAATAGAACAGTGCCAATAGAACAAGAACAAAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAAACAAAACAAAACAAAAAA
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                          TCCGACCAGCAGACATCAAAGTGGTGGCCGCCCTGGGTGACTCTCTGACTACAGCAGTGG
                                                                                     GAGCTCGACCAAACAACTCCAGTGACCTACCCCACATCTTGGAGGGGGCTCTCTTGGAGCA
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Pred. No. 0;
0; Mismatches
PRIOR FILING DATE: 2001-12-03
PRIOR PLING DATE: 2001-12-03
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-27
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Best Local Similarity 86.1%;
Matches 1535; Conservative
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US-10-092-900A-81
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APPLICANT: Hyseq Inc.

TITLE OF INVENTION: NO. US20040053248Alel Nucleic Acids and Polypeptides

TITLE OF INVENTION: NO. US20040053248Alel Nucleic Acids and Polypeptides

FILE REFERENCE: 784PCT

CURRENT APPLICATION NUMBER: US/10/296,115

PRIOR APPLICATION NUMBER: US/9/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US/9/552,317

PRIOR APPLICATION NUMBER: US/9/552,317

PRIOR APPLICATION NUMBER: US/9/552,317

PRIOR APPLICATION NUMBER: US/9/552,317

PRIOR PRIOR PRIOR DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 14778

SEQ ID NO 600
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Pred. No. 3.7e-170;
0; Mismatches 1;
                                                                                                                                   ; Sequence 600, Application US/10296115; Publication No. US20040053248A1; GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 668; Conservative (
                                                 CTCTGAGGA 942
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794 CTCTGAGGA 802
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CRGANISM: Homo sapiens
US-10-296-115-600
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                                                                                           Sequence 73, Application US/10276774

Sequence 73, Application US/10276774

Publication No. US20040053245A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT APPLICATION NUMBER: 09/560,875

PRIOR APPLICATION NUMBER: 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-02-03

PRIOR FILING DATE: 2000-02-03

PRIOR FILING DATE: 2000-02-03

SOFTWARE: Custom

SEQ ID NO 73

LENGHH: 802
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                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                     Query Match
36.4%; Score 667.4; DB 17;
Best Local Similarity 99.9%; Pred. No. 3.7e-170;
Matches 668; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-10-276-774-73
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   421 CTTCACTGCCCTCTGCCCCAGCCACTCCCGGCCACCAGGACATGCTTCAATGCCTGGTGC 480
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SGequence 1191, Application US/09764891

SCHORLEAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

CURRENT PRILIGATION NUMBER: US/09/764,891

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 10231

SOFTWARE PatentIN Ver. 2.0

SEQ ID NO 1391

LENGTH: 572
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                                                                                                                  CTCCTGGAATGGATACATTTAAATAAAGTCCAAAGCTATTTTA 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: SITE
LOCATION: (375)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (529)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
US-09-764-891-1391
                                         1698
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                   Gaps
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                                                                                                                                                                                                                                                         APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PAI31P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
FRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR APPLICATION NUMBER: DCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
SOFTWARE: PATENTIN ON SEQ ID NOS: 2876
SOFTWARE: PATENTIN VEY: 3.1
SEQ ID NO 323
LENGTH: 861
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31.3%; Score 575; DB 17;
Best Local Similarity 99.1%; Pred. No. 4.2e-145;
Matches 578; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature

: LOCATION: (846)

: OTHER INFORMATION: n equals a,t,g, or

US-10-264-237-323
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US-10-264-237-323
; Sequence 323, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURE:
NAME/KRY: misc feature
LOCATION: (802)
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OTHER INFORMATION: n equals a,t,g,
                                                                       CTCTGAGGA 942
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CTCTGAGGA 802
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ORGANISM: Homo sapiens
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Score 210.6; DB 17; Length Pred. No. 3.3e-46; 0; Mismatches 374; Indels

11.5%;

11.5% Query Match Best Local Similarity 55.1% Matches 492; Conservative

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; LOCATION: (311)..(1241) US-10-092-900A-83

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APPLICANT: Zhong, Haihong
APPLICANT: Alsobrook, John P.
APPLICANT: Ispley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same FILE REFRENCE: 21402-290C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 768
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CURRENT PAPLICATION NUMBER: US/10/092,900A
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: USSN 60/274,322
PRIOR FILING DATE: 2001-03-08
PRIOR PELICATION NUMBER: USSN 60/283,675
PRIOR APPLICATION NUMBER: USSN 60/283,092
PRIOR APPLICATION NUMBER: USSN 60/274,281
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR PRILICATION NUMBER: USSN 60/325,681
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: USSN 60/294,899
PRIOR PRING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: USSN 60/294,899
PRIOR PRING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR PRING DATE: 2001-03-30
PRIOR PRING DATE: 2001-03-30
                                                                                                                           APPLICANT: Padigaru, Muralidhara APPLICANT: Spytek, Kimberly A. APPLICANT: Spenoy, Surseh G. APPLICANT: Taupler Jr., Raymond J. APPLICANT: Pena, Carol E.A. APPLICANT: Li, Li
                                             ; Sequence 83, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Gorman, Linda
Miller, Charles E.
Kekuda, Ramesh
Patturajan, Meera
Gangolli, Esha A.
Vernet, Corine A.M.
Guo, Xiaojia Sasha
Tchernev, Velizar T.
Fernandes, Elma R.
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Malyankar, Uriel M.
Gerlach, Valerie
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Gusev, Vladimir Y.
Ji, Weizhen
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Anderson, David W.
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ORGANISM: Homo Bapiens
FEATURE:
NAME/KEY: CDS
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LENGTH: 1624
RESULT 10
US-10-092-900A-83
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                                                                                                                                  662 AACCCTTACCTCCTTGGCTTCTCTACCAGCACCTGGGAGGGGAC------AGCAGGA 712
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602 ATTGGAGGAGATGGGAACTTGGAGACTCACACCACACTGCCCAACATTCTGAAGAAGTTC
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US-10-094-749-390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
FILE REPERENCE: 21272-003
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                722 CAGTGCTCTCTGGAACAATATGCTGGAGCCTGTTGGCCAGAAGACGACTCGTCATAAGTT
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                              GCATGGCATCTCCAGTTTCTCCTACTGGCACCAATACACACAGCGTGAGGACTTTGCGGT
                                                                           542 GGAGAAGACCCACCAACTGATTGAGAGTGGGCGATATGACACAAGGGAAGATTTTACTGT
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Pred. No. 4.4e-14;
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US-10-357-930-52986/c
; Sequence 52986, Application US/10357930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 257, Application US/10276774; Publication No. US20040053245A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.0%;
Best Local Similarity 59.1%;
Matches 179; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 ccaggagaaaarcracrgcccaaggargarccrcaggrcrcrgrgrcccrgrgrcccr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             482 GAAGTTTGATGATAACTCAACAGAACTTGCTACCCTCATCGAATTCAACAAGAAGTTTCA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 AATAACCCTGTTTATAGGCGGCAATGACCTCTGTGATTTCTGCAATGATCTGGTCCACTA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 TICTCCCCAGAACTICACAGAACATIGGAAAGGCCCTGGACAICCTCCAIGCTGAGGI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GCAGGACTAAATGTGGCAGCGGAAGGGGCCAGAGCTAGGGACATGCCAGGCCCAGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17; Length 2477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1006 AGCCGGGAAATGTGCCATGCTGGCAGCTCAGAACAACTGCACTTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.2%; Score 186.8; DB 17; Length 54.7%; Pred. No. 1.1e-39; ive 0; Mismatches 332; Indels
                                                                                                                                                                                                                                                                               APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NACHIKO
APPLICANT: SEKI, NACHIKO
APPLICANT: SCHIKAWA, TSUTOMU
APPLICANT: OYSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2010-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2010-09-14
NUMBER OF SEQ ID NOS: 3381
SENGTH: 2477
                                                                                                                                                                                                                                                                IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NACHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                 ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
SOGAI, TAKAO
SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 54.7
Matches 427; Conservative
                                                                 WAKAMATSU, AI
SATO, HIROYUKI
                                                                                                                                                                                                                                            NAGAI, KEIICHI
                                                                                                                                                                                                                   OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          707
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APPLICANT:
APPLICANT:
APPLICANT:
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8 8 8

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TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 126452, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION

APPLICANT: La Rosa, Thomas J.

APPLICANT: Exovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT PLING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 126452

LENGTH: 568
                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
ITILE OF INVENTION: HOWEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HURAN PROSTATE CANCER
FILE REFERENCE: MR-0079GV
CURRENT PELLIGO DATE: 2003-02-04
PRIOR PELLING DATE: 2003-02-16
PRIOR PELLING DATE: 2000-02-16
PRIOR PELLING DATE: 2000-03-16
PRIOR PELLING DATE: 2000-03-16
PRIOR PELLING DATE: 2000-03-16
PRIOR PELLING DATE: 2000-05-25
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-30
PRIOR PELLING DATE: 2000-07-18
PRIOR PELLING DATE: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 GACATCAACCTGGAGAAAGACTGGAAAGCTGGTCACACTCTTCATTGGGGTCAACGACTTG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rercarracteres de la recensión de la recensión
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74.7%; Pred. No. 0.00011;
tive 0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6%; Score 83.8; DB 18;
88.3%; Pred. No. 3.9e-12;
tive 0; Mismatches 12;
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, OTHER INFORMATION: Clone ID: MRT4577_46792C.1
US-10-425-115-126452
Publication No. US20040259086A1 GENERAL INFORMATION:
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Best Local Similarity 74.7
Matches 71; Conservative
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Best Local Similarity 88.3<sup>3</sup>
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
US-10-357-930-52986
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ORGANISM: Zea mays
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APPLICANT: Allory Wendy M. APPLICANT: Allory Mendy M. APPLICANT: Allory Wendy M. APPLICANT: Zlotnik, Albert Ginsburg, Wendy M. APPLICANT: Zlotnik, Albert TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators FILE REFERENCE: 0582.0193.NPUS01

CURRENT APPLICATION NUMBER: 001429,739

PRIOR FILING DATE: 2002-11-26

PRIOR FILING DATE: 2002-11-26

PRIOR FILING DATE: 2002-11-26

PRIOR FILING DATE: 2002-11-26

PRIOR FILING DATE: 2003-11-26

PRIOR FILING DATE: 2003-11-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 écrgréacriricaracretectragrétrasabaaaarakaacrégagarabaaaaaaaa 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 crideceridericaecerangriderecerarecrarecresidadecerrirreaadirie 188
CITCITCCAGGCCIAIGCTCCTGGAATGGATACAITTAAATAAAGTCCAAAGCTAITTTA 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 Acceradaacaacadaceccccrrccarcectraaceccaaaaccaracacadac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1613 ACCCTARACTCCCTATAGCCACTCTTCACCGCCCTCTGCCCCAGCCACTCCCGGCCAC
                                                              172 ciririraaaccrirraaaccccaardggrarririraarccaarrccaagrirrira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.1%; Score 56.2; DB 18;
Best Local Similarity 52.9%; Pred. No. 0.0001;
Matches 118; Conservative 0; Mismatches 105;
                                                                                                                                   112 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: March 27, 2005, 12:54:56 Job time : 1074.69 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | FEATURE:
| NAME/KEY: misc feature
| LOCATION: (254)...(255)
| OTHER INFORMATION: n is a, c, g, or t
| US-10-723-860-3816
                                                                                                                                                                                                                                                                                                                                                      sequence 3816, Application US/10723860 publication No. US20040253606A1 GENERAL INFORMATION:
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BX354649 4058544 B 969472 MA

AL569658

Mus muscu

BX451441

CK950790
AWV52883
AWV528838
BX354649
CK834245
CK846912
BV731604
BX731604
BX731604
BX65117
BE137831
BE137831
BE137831
BE137831
BE137831
AA646625
AA461625

ug68b11.y 184141 MA BX517602

603068631

603345949 603290988

4095904 B

ALIGNMENTS

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Direct Submission

Listed (20-2014) Genoscope - Centre National de Sequencage :

Submitted (20-2014-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen:

1. 1661

| Location/Qualifiers | Location/Qu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TR612785 1661 bp mRNA linear HTC 21-JUL-2004 cull-length cDNA clone CSODC023YA08 of Neuroblastoma Cot 25-normalized of Homo sapiens (human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTTGAACCACTTGGAAGCAAAACAGAGCCCTGGACCTGAGAGCAGAGATGCCCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
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/tissue type="Neuroblastoma
/plasmid="pCMVSPORT_6"
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Pred. No. 0;
0; Mismatches
                                                                    AL569658
BX354649
CK834245
                 BM923066
CK950790
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BU743739
BY731604
AK087596
BX451441
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BE684057
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AA461827
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HTC; CNSLT_cDNA.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 97.4%;
Matches 1493; Conservative (
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BU663311 UI-CF-ECI
BU68331 UI-CF-ECI
BM14799 UI-H-EIO-
BM714799 UI-E-EJO-
AM467395 heIOel2.x
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PRODG1GID
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hel0e12.x
UI-E-EJ0-
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                                                                                                                 March 26, 2005, 13:10:00 ; Search time 5913.96 Seconds (without alignments) 11810.698 Million cell updates/sec
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BX369782 BX369782
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Gaps

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DB 3;

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1374 1269 1434 1329 1389		RESULT 2 CR600701 LOCUS	AUTHORS Genoscope. TITLE Direct Submission JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : JOURNAL SUBMITTE (20-JUL-2004) Genoscope - Centre National de Sequencage : JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) - Web : www.genoscope.fr) - Web : www.genoscope.fr) - Web : www.genoscope.fr) - Web : www.genoscope.fr) - Web : www.genoscope	division of Invirtogem. FEATURES 1. 1561 SOURCE Corganism="Homo sapiens"	Query Match 58.9%; Score 1081; DB 3; Length 1561; Best Local Similarity 100.0%; Pred. No. 7.5e-253; Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
334 CTGTCCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACAGTACCC 393 189 CTGTCCCACTCAGATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCC 248 189 CTGTCCCACTCAGATGAGCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCC 248 394 CATCAAGCCAGCCATTGAGAACTGGGGCAGTACTTCCTGTGTACAGAGTGGAAGGCTTC 453 249 CATCAAGCCAGCCATTGAGAACTGGGGCAGTACTTCCTGTGTACAAGTGGAAGGCTTC 308 249 CATCAAGCCAGCCATTGAGAACTGGGGCAGTACACTACAGAGTGGTGGGAAGGCTTC 308 454 CAATAGTGTTCCAACCTGTCCACCAGCTCCAACCAGCAGAACTGAAGTGGTGGGCGC 513		614 CIGOGAGGGACAGCAGACTAAATGTGGCAGCAGAGGCCCAGAGCTAGGGACATGCC 608 549 CTGGGAGGGACAGGCACTAAATGTGGCAGCAGAGGCCCAGAGCTAGGGACATGCC 608 549 CTGGGAGGGACCTGGGACTAAATGTGGCAATGAAAAAGGCCCCGACATCAACCTGGAGAA 813 754 AGCCCAGGCCTGGGAACTGAATGAAAAAAAAAAAAAAAA		1134 CCTACTGGCACCAATACACAGGGGGAGGACTTTGCGTTGGTTG	STITTCACTTCTCAGACCGGGGCATGCCGAGATGGCCATCGCACTTTGGGTGGG

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/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE013YE22
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone="CS0DE013YE22"
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                     GAATGAAAAACAGCCCCGACATCAACCTGGAGAAAAGACTGGAAGCTGGTCACACTCTTCA
                                                                                                                                                TTGGGGTCAACGACTTGTGTCATTACTGTGAGAATCCGGAGGCCCACTTGGCCACGGAAT
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Homo sapiens (human)

Homo sapiens (bordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Homo.

Amamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ACE 1 (Dases 1 to 935)

NH-MGC http://mgc.nci.nih.gov/.

B NH-MGC http://mgc.nci.nih.gov/.

B National Institutes of Health, Mammalian Gene Collection (MGC)

E National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapber-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Preparation: Life Technologies, Inc.

Clone distribution: MC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMJ3555 row: n column: 23

High quality sequence stop: 532.

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/dev stage="adult, 36 yr"
/lab_host="adult, 36 yr"
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Technologies."
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Best Local Similarity 93.1%; Pred. No. 1.7e-176;
Matches 860; Conservative 0; Mismatches 56;
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1 (bases 1 to 925)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30371419.
                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAAGAAAGTGAACTGGAACCTCCAGCATGGCATCTCCCAGTTTCTCCTACTGGCACCAA
                                                                              TCACACTCTTCATTGGGGTCAACGACTTGTGTCATANCTGTGAGAATCCGGTAGGCCCCC
                                                                                                                                            CACATCCAACAGGCCCTGGACATCCTCTGAGGAGCTCCCAAGGGCTTTCGTCAACGTG
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2 rue Gaston Cremieux, CP 5706 - 91057 BVRX cedex - FRANCE
Email: seqref@genoscope.cns fr. Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five
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Genoscope - Centre National de Sequencage
Z rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and it belongs to a clone representative of this cluster. For more information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?s=CSOBAI005ZA12_CSO0473_2&c=1474.f
                                                                                                                 GCAGGAGAGGTGG---CCGGAGGGAAGATCCTCCAATGAGCCTGCGCACTGTGGCCCTCT 1592
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A COT 25-NORMALIZED Homo sapiens
                                                                                                                                        /organism="Homo sapiens"
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primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (bases 1 to 903)
Li, W.B., Gruber.C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
ACAGCCGACTGCTCCCAGACCAGGCTGAAGAAACCCCCGGAGGGCTCCTACTGGGCTGTCC
                                                         TTCTGAAGAAGTTCAACCCTTACCTCCTTGGCTTCTCTACCAGCACCTGGGAGGGGACAG
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BX349938 Homo sapiens NEUROBLASTOMA COT 25-NORM
CDNA clone CSODC023YA08 3-PRIME, mRNA sequence.
BX34938
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Pred. No. 1.4e-174;
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Genoscope - Centre National de Sequencage
Z rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Z rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Esmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Esmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
end cariched, double-strand cDNA was digested with Not I and cloned
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoP V sites of the pcMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/note="lst strand cDNA was primed double-strand cDNA was primer. Five prime end enriched, double-strand cDNA was digested with Noil and cloned into the Noil and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Catarrhini; Hominidae; Homo.
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                                                                                   CAACATGCTGGAACCAGTGGGCCGCAAGACTACCTCCAACAACTTCACCCACAGGCGGAGG
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30441506.
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llarity 93.3%; Pred. No. 3.3e-159;
Conservative 0; Mismatches 14;
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                                 end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                             1474.f, and it belongs to a clone representative of this cluster. For more information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?e=CSOBAIOO5ZA12_CSO0473_1&c=1474.f
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/tissue type="NREMORLASTOMA COT 25-NORMALIZED"
/tissue type="NREMORLASTOMA COT 25-NORMALIZED"
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/clone lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/clone lib="the" or no sapiens of primed with a Not1-oligo(dI)
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSFORT 6 vector. Library was normalized."
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Pred. No. 6.5e-167;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/GLOBEL 11b="NHE MGC 118"
//GLOBEL 11b="NHE MGC 118"
//GLOBEL 12b="NHE MGC 118"
//GLOBEL 12b="NHE MGC 118"
//GLOBEL 12b="NHE MAN SOURCE leukcytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
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                       can
   DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.B. Consortium/LLNL at: http://mage.llnl.gov
http://mage.llnl.gov
Plate: LLAM12769 row: i column: 24
High quality sequence stop: 626.
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Pred. No. 3.1e-154;
0; Mismatches 6;
                                                                                                               Query Match 36.9%;
Best Local Similarity 98.5%;
Matches 736; Conservative
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NIH-WGC http://mgc.nci.nih.gov/.
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Contact: Robert Strausberg, Ph.D.

Email: capabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Pred. No. 3.3e-142;
0; Mismatches 3;
and 380-383
TAG LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"
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/mol_type="mRNA"
/db xrefe="texon:9606"
/clone="UL-CF-EC1-ace-k-16-0-UI"
/tissue_type="Lung"
/dev stage="Adult and Fetal"
/done_lib="UL-CF-EC1"
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University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 366 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Clone Distribution: Researchers may obtain clones from Research
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
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/organism="Homo sapiens"
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: brain; Vector: prime and vice range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note:
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                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: Limilaty row: g column: 09
High quality sequence stop: 808.
Location/Qualifiers
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                                                       Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 823)

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/lab host="DH10B"
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/db_xref="taxon:9606"
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/done lib="NCI_CAPP EIO"
//done lib="NCI_CAP CA447656 625 bp mRNA linear BST 08-NOV-2002 UI-H-EIO-ayf-c-03-0-UI.81 NCI CGAP_EIO Homo sapiens cDNA clone UI-H-EIO-ayf-c-03-0-UI 3', mRNA sequence. Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained 872 932 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 625) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), 814 AGACTGGAAGCTGGTCACACTCTTC-ATTGGGGTCAACGACTTGTGTCATTACTGTGAGA ATCCGGAGGCCCACTTGGCCACGGAATATGTTCAGCACATCCAACAGGCCCTGGACATCC from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this CDNA
Sequence: 1-24, AT_rich#Low_complexity
Seq primer: MI3 FORWARD
POLYA=Yes. /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H=EIO-ayf-c-03-0-UI"
/tismu_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B_(Life_Technologies)"

us-09-778-961-1.rst

```
Chorold"

/dev stage="fetal and adult"
/dev stage="fetal and adult"
/deb host="DH10B (Life Technologies) (TI phage resistant)"
/donelib="UI-E-EJO"
/clonelib="UI-E-EJO"
/clonelib="UI-E-EJO"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site_2: Not I; modified polylinker; Site 1: EcoR I; Site_2: Not I; modified polylinker; Site 1: EcoR I; Site_2: Not I; modified polylinker; Site 1: EcoR I; Site_2: Not I; modified polylinker; Site 1: EcoR I; Site_2: Not I; site and soares, Genome Research, ergoding to Bonaldo, Lennon and Soares, Genome Research, ergand cDNA was ligated to an EcoR I adaptor, digested stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector: The oligonalcleotide used to prime the synthesis of vector: The oligonalcleotide used to prime the synthesis of first-strand cDNA contains a library are sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGCATAAGTG; retina, CCGCGG; Retina AATGCCGCAT, optic nerve, CCATTAAGTG; retina, CCGCGG; Retina Foveal and Macular, GTCC; RPB and Choroid, ACCTA. This Foveal and Macular, GTCC; RPB and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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University of Iowa 315 8260
Tel: 319 335 8250
Fax: 319 335 9526
Fax: 319 335 9560
Fax: 319 315 9562
Email: bento-goares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
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Seg primer: M13 Reverse.
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: 'two approaches to facilitate gene
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                                                                                              Length 625;
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Pred. No. 3e-141;
0; Mismatches 1.
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Matches 624; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM Homo sapiens (Taniata, Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. I (Dases 1 to 583)

8 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Monce,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Materston,R. and Wilson,R. Tonpublished (1997)

L. Unpublished (1997)

Contact: Wilson RK. Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fas: 314 286 1800

Fas: 314 286 1800

Email: est@watson.wustl.edu
                                                                                                     GACACTGACCTCACCTTCTTCCGAGGACTGTTTTCACTTCTCAGACCGCGGGCATGCC 1285
                                                                                                                                                                           GAGATGGCCATCGCACTCTGGAACAACATGCTGGAACCAGTGGGCCGCAAGACTACCTCC 1345
                                                                                                                                                                                                                                                                                                                                                                  AA418082 Sares NHHMPu_S1 Homo sapiens cDNA clone IMAGE:7677777 3'similar to SW:PHLX_RABIT Q05017 PHOSPHOLIPASE ADRAB-B PRECURSOR ;,
                                                    TTTGCGGTTGTGGTGCAGCCTTTCTTCCAAAACACACTCACCCCACTGAACGAGAGGG 480
                                                                                                                        AACCTCCAGCATGGCATCTCCAGTTTCTCCTACTGGCACCAATACACACAGGGGGGAC 420
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/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 477.
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/db_xref="taxon:9606"
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616 bp mRNA linear EST 24-FEB-2000 heloel2.xl NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918638 3' similar to SW:FHIX FABIT 005017 PHOSPHOLIPASE ADRAB-B PRECURSOR contains MER22.tl_MER22 repetitive element ;, mRNA sequence.
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Unpublished (1997)

Unpublished (1997)

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University
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Clone distribution: NCI-GGAP clone distribution information can left ound through the I.M.A.G.B. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image.html
Seq primer: -400P from Gibco
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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National Cancer Institute, Cancer Genome Anatomy Project
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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/organism="Homo sapiens"
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/db xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGGGTCCTCACCCTAAACTCCCTATAGGCACTCTTCACCGCCCTCTGCCCCAGCCAC 1662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1303 CIGGAACAACAIGCIGGAACCAGIGGGCCGCAAGACIACCICCAACAACIICACCCACAG 1362
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                                                                                                                                                                                                                                                                                                                                                                                                          "Jab host="DH10B" | CAD CML1" | Colone | 11b="NCI CGAP CML1" | Colone | 11b="NCI CGAP CML1" | Colone | CAD CMV-SPORT6; Site_1: | CAD CMV-SPORT6; Sit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGAGCCAAACTCAAGTGCCCCTCTCCTGAGGCCCTTACCTCTACACCCTGCGGAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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Pred. No. 3.8e-128;
0; Mismatches 22; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                      /organism="Homo sapiens"
                                  High quality sequence stop: 422.
Location/Qualifiers
                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2918638"
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ilarity 96.3%;
Conservative (
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BU739708/c
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Matches
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Chorola"

(dev grage="fetal and adult"

/dev grage="public life Technologies) (Ti phage resistant)"

/dev bost="DHIOB (Life Technologies) (Ti phage resistant)"

/dlone lib="UI-B-EJO"

/dote="Cragan: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site_2: Not I;

modified polylinker; Site 1: EcoR I; Site_2: Not I;

UI-B-EJO is a subtracted cDNA library constructed

UI-B-EJO is a subtracted cDNA library constructed

scoroling to Bonaldo, Lennon and Soares, Genome Research, escoroling to Bonaldo, Lennon and Soares, Genome Research, stranded cDNA was ligated to an EcoR I adaptor, digested with an oligo-dT primer containing a Not I site. Double with Not I, and clonded directionally into PT7T3-Pac vector. The oligonucleotide used to prime the synthesis of vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library are: fetal eyes, sequence tags for this library are: fetal syes

ROGARIPAGTS, retina, CGGGS, Retina AAGGCGAT; optic nerve, CGTCT, RPE and Choroid, ACCTA. This Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This Several and Macular, GTCC; RPE and Choroid, ACCTA. This TAG_IDSUB=RPE and Choroid directive (NEI).

TAG_IDSUB=RPE and Choroid directive.

TAG_IDSUB-RPE and Choroid directive.

TAG_IDSUB-RPE and Choroid directive.
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/clone="UI-E-EJO-ahs-f-21-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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99.8%; Pred. No. 4.4e-127;
:ive 0; Mismatches 1;
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GI:23678342

BU739708 BU739708.1

ACCESSION VERSION

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507 ACATGCTGGAACCAGTGGCCGCAAGACTACCTCCAACAACTTCACCCACAGCCGAGCCA 448

Search completed: March 27, 2005, 03:40:32 Job time : 5924.96 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

March 25, 2005, 14:18:06 ; Search time 176 Seconds (without alignments) 1037.221 Million cell updates/sec

1 MRELVGSGRYDTQEDFSVVL.....RCRRGGRREDPPMSLRTVAL 472 US-09-778-961-2 2518 Title: Perfect score: Sequence:

BLOSUM62

Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

Searched:

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_16Dec04:* geneseqp20048:* geneseqp2002s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Abp53556 Human pho	Abb09555 Human lip	Aae34440 Human lip		Aae22860 Human pho	Human	1 Novel	Adn61817 Human nov	Abu65081 Human NOV	Adh42427 Novel hum	Adn61813 Human nov	Adol8815 Human lip	Aaw30751 Rat phosp	Human	Abb11053 Human pho	Adh13664 Human ENZ	Aae34448 Human lip	Ado18816 Human lip	Adn24372 Bacterial	Adn22922 Bacterial	Abb89352 Human pol	Aam95420 Human rep	Human	Abb71556 Drosophil	Abb65406 Drosophil
ID	i	ABB09555	AAE34440	ABB09556	AAE22860	ABU65083	ADH42431	ADN61817	ABU65081	ADH42427	ADN61813	AD018815	AAW30751	AAM25824	ABB11053	ADH13664	AAE34448	AD018816	ADN24372	ADN22922	ABB89352	AAM95420	ABB96111	ABB71556	ABB65406
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Length	472	1458	1458	1458	1216	1423	1423	1423	1419	1419	1419	1433	1450	267	267	937	696	1004	382	414	101	148	148	424	447
& Query Match	100.0	99.0	99.0	98.8	98.1	92.6	92.6	94.8	92.8	92.8	92.8	92.7	68.1	47.1	47.1	35.1	35.1	35.1	23.8	21.9	20.9	20.9	20.9	20.7	20.0
Score	2518	2492	2492	2488	2469	2407	2407	2387	2336.5	2336.5	2336.5	2334.5	1715.5	1185	1185	884.5	884.5	œ	S.	u,	527	527	527	521	504
Result No.	1		m	4	Ω.	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Ada54461 Human pro Abu65082 Human NOV Adh42429 Novel hum Adn61815 Human nov		Bacter Novel	Adel0214 Human bon Abb11237 Human pho Adr41635 Lipid acy	Human Human	Abm82537 Human dia Abm82536 Human dia Abm82535 Human dia	Abm82534 Human dia
ADA54461 ABU65082 ADH42429 ADN61815	ADN22763 ADN22763 ADN23870	ADN22508 ABG02997	AAE10214 ABB11237 ADR41635 ADR41585	AA030422 AA030421	ABM82537 ABM82536 ABM82535	ABM82534
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465.5 456.5 456.5	452.5	324.5	233.5 233.5 113	108	108 108 108	108
222 284 284	3310	1 W W C	3 3 3 4 4 4 8 9) 4 4 . , O L (4 4 4 2 6 4	45

ALIGNMENTS

Di Francesco V, Beasley EM; Human; phospholipase; enzyme; chromosome 2. Human phospholipase protein SEQ ID NO:2. RESULT 1

New human phospholipase proteins, useful for the development of human therapeutics and diagnostic compositions, drug screening assays, tissue typing and pharmacogenomic analysis.

The present sequence represents a human phospholipase protein (1) located on chromosome 2. (1) can be used for identifying agents that modulate its function or activity where the agent is useful for treating a disease or condition mediated by a the human phospholipase protein. (1) peptides can be used in substantial and specific assays related to functional information of the peptide sequences, to raise antibodies or to elicit immune response, as reagents in assays that determine the levels of protein in biological fluids, and as markers for tissues where the corresponding protein is expressed. Nucleotide sequences encoding (1) can be used as probes, primers and chemical intermediates in biological assays, for constructing recombinant vectors, and expressing antigenic portions of the protein. (1) and nucleic acid molecules encoding it can be used in the identification of therapeutic proteins and may serve as

INC. Ŗ

(LEXI-) LEXICON GENETICS

Turner

Miranda M,

2002-599797/64.

N-PSDB; ABQ77623.

24-JAN-2001; 2001US-0264049P.

2002WO-US001715

22-JAN-2002;

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                                                                                                                                                                                                                                                                                                      Human; lipase; chromosome 2; phospholipase B homologue; thyroid; brain; inflammatory disease; proliferative disease; infectious disease; clotting disorder; cancer; drug screening; mental disorder; NHL; diagnostic reagent; clinical trial monitoring; cosmetic; nutriceutical; mutation detection; gene expression analysis; transgenic animal; nootropic; cytostatic; antinflammatory; single nucleotide polymorphism;
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                                                                                                                                                                                                                                                                                                                                                    CFHFSDRGHAEWAIALWNNMLEPVGRKTTSNNFTHSRAKLKCPSPESPYLYTLRNSRLLP
                                                                                                                                                                                                                                                                                                                                                                                           models or targets for the development of human therapeutic agents that modulate phospholipase activity in cells and tissues that express the phospholipase, such as in kidney, blood, lung, brain glioblastomas, prostate, colon or leukocytes
                                                                                                                                                              61 PLRTPRNSNYTYPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTT
                                                                                                                                                                           AVGARPNINSSDLPTSWRCLSWSIGGDGNLETHTTLPNILKKFNPYLLGFSTSTWEGTAGL
                                                                                                                                                                                                                    NVAAEGARARDMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLAT
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                                                                                                   Gaps
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                                                                              472;
                                                                              Length
                                                                                                    Indels
                                                                              100.0%; Score 2518; DB 5;
100.0%; Pred. No. 6e-232;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB09555 standard; protein; 1458
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SNP; gene therapy; enzyme
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                                                                                                      472; Conservative
                                                                                    Query Match
Best Local Similarity
                                                               Sequence 472 AA;
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The invention relates to a novel human lipase (NHL, ABB09555, ABB09556)

CC and to nucleic acids encoding it (ABQ77623, ABQ77624). The NHL has

CC structural similarity with animal lipases, particularly phospholipase B.

cc structural similarity with animal lipases, particularly phospholipase B.

CC in conjunction with human thyroid and brain cDNAs. The NHL gene is

In conjunction with human thyroid and brain cDNAs. The NHL gene is

cc in conjunction with human thyroid and brain cDNAs. The NHL gene is

located on chromosome 2, and contains a C/T polymorphism at position at

cc the open reading frame (ORF), resulting in an Ala/Val substitution at

cc the open reading frame (ORF), resulting in an Ala/Val substitution at

cc treating disorders such as inflammatory or proliferative disease.

cc infections disorders and inflammatory or proliferative disease.

cc infections disorders, and cancer. They can also be used

infection disorders, and disponders, and cancer. They can also

cc medical disorders, and ingnostic reagents, in clinical trial

cc medical disorders, and nutriceutical applications. NHL

conclotides can additionally be used in the detection of disease.

cucleotides can additionally be used in the detection of disease.

crecombinant expression of NHL, to generate transgenic animals, in gene

crecombinant expression of NHL, to generate transgenic animals, in

cc therapy, and as part of ribozyme and/or triple helix sequences useful in

cc therapy, and as part of ribozyme and/or triple helix sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1314
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                                                                                                                                                           Polymucleotides encoding human lipases that are structurally related to animal lipases, particularly phospholipase B, useful for drug screening, diagnosis and in gene therapy of biological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQR
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Pred. No. 1.2e-228;
0; Mismatches 0;
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Best Local Similarity 93.7'
watches 472; Conservative
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/note= "Val raplaces Ala in a polymorphic variant (ABB09556)"

Location/Qualifiers

Key Misc-difference

WO200259328-A1

01-AUG-2002.

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1375 TSNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLYWAVPVAAGVGLVVGIIG 1434
                                                                                                                                                                                                          Human; lipid-associated molecule; LIPAM; cardiovascular disorder; stroke; arteriovenous fistula; atherosclerosis; hypertension; Raymaud's disease; aneturysm; congestive heart failure; thrombophlebitis; anglina pectoris; ischaemic heart disease; themsine heart disease; peptic oesophagitis; gastrointestinal disorder; lipid metabolism disorder; Crohn's disease; nausea; peptic ulcer; fatty liver; Fabry's disease; Gaucher's disease; diabetes mellitus; hyperlipidaemia; hypercholesterolaemia; epilepsy; acquired immunodeficiency syndrome; anaemia; Alzheimer's disease; dementia; prion disease; Creuzfeldt-Jakob disease; leukaemia; cancer; adenocarcinoma; lymphoma; melanoma; myeloma; garcoma; gene therapy;
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note= "Lipolytic enzyme G-D-S-L family serine active-
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'note= "Lipase/acylhydrolase with GDSL-like motif"
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/note= "Transmembrane domain"
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|abel= Signal-peptide
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/label= Signal-peptide
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'label= Signal-peptide
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741. .751
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/label= 6
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17-MAY-2002; 2002WO-US015688.

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The present invention relates to novel human lipid-associated molecules invention are useful for treating diseases or conditions associated with decreased expression of functional LIPAM. The antagonist is useful for treating a disease or condition associated with the overexpression of treating a disease or condition associated with the overexpression of treating a disease or condition associated with the overexpression of cardiovascular disorders (e.g. arteriovenous fistula, atherosclerosis, hypertension, Raynaud's disease, aneurysms, varicose veins, congestive beart failure, thrombophlebitis, angina pectoris, ischaemic heart disease or rheumatic heart disease), agstrointestinal disorders (e.g. peptic or rheumatic heart peptic ulcer or Crohn's disease), lipid metabolism disorders (e.g. fatty liver, Fabry's disease, Gaucher's disease, diabetes cesophagitis, nausea, peptic ulcer or Crohn's disease, diabetes consiliammatory disorders (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's disease), neurological disorders (e.g. acquired immunodeficiency syndrome, critiammatory disorders (e.g. acquired immunodeficiency syndrome, critiametory disorders (e.g. acquired immunodeficiency syndrome, creutzfeldt-Jakob disease) or cancers (e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma or sarcoma). They are also used in gene therapy and protein replacement therapy. The present sequence is human or strong therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                     New human lipid-associated molecule (LIPAM) proteins and polynucleotide useful for diagnosing, treating or preventing cardiovascular disorders (e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or
                                                                                                                                                                                                                                                                             Lee
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I Y, Gandhi AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Das D, Nguyen DB, Yao MG, Arvizu CS, Lu Y, Gandhi
Elliott VS, Ramkumar J, Lal PG, Lu DAM, Lee EA,
J Tribouley CM, Kable AE, Swarnakar A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 56; Page 137-141; 171pp; English.
                                                                             06-JUL-2001; 2001US-0303404P.
24-AUG-2001; 2001US-0314754P.
24-AN-2002; 2002US-0351262P.
29-MAR-2002; 2002US-035199P.
                    2001US-0292242P.
2001US-0293726P.
                                                            2001US-0295346P
                                                                                                                                                                                                                                Yue H, Azimzai Y,
Das D, Nguyen DB
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Matches 472; Conservative
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                 18-MAY-2001; 25-MAY-2001; 201-JUN-2001; 2
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Walia NK, Da
Griffin JA,
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Human, phospholipase-like enzyme; cancer; inflammation; Pick's disease; cardiovascular disorder; central nervous system disorder; brain injury; chronic obstructive pulmonary disease; cerebrovascular disease; dementia; Alzheimer's disease; Parkinson's disease; corticobasal degeneration; motor neuron disease; Huntington's disease; Creutzfeld Jacob dementia; schizophrenia; Korsakoff's psychosis; pain; epilepsy; multiple sclerosis; sciatica; stroke; age associated memory impairment; allergy; asthma; allergic rhinitis; hay fever; atopic dermatitis; cardiovascular disease;
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or medical disorders, as diagnostic reagents, in clinical trial monitoring and in cosmetic and nutriceutical applications. NHL nucleotides can additionally be used in the detection of disease-secolated mutations, in the analysis of gene expression, for the recombinant expression of NHL, to generate transgenic animals, in gene the modulation of NHL, to generate transgenic animals, in gene the modulation of NHL analysis. The present sequences useful in the val 1318 variant of NHL on the present sequence represents the val 1318 variant of NHL was derived from the the information given on page the specification, but was derived from the the information given on page 18 and the Ala 1318 NHL variant (ABB09555) given in the sequence listing
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Pred. No. 2.8e-228;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                         MRELVGSGRYDTQEDFSVVLQPFFQNIQLPVLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1435 TVVWRCRRGGRREDPPMSLRTVAL 1458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human phospholipase-like enzyme.
                                                                                                                                                                                                                                                                                                                    Query Match 98.8%;
Best Local Similarity 93.5%;
Matches 471; Conservative (
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                                                                                                                                                                                                                          1314
                                                                                                                                                                                                     TSNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLYWAVPVAAGVGLVVGIIG 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; lipase; chromosome 2; phospholipase B homologue; thyroid; brain; inflammatory disease; proliferative disease; infectious disease; clotting disorder; cancer; drug screening; mental disorder; NBL; diagnostic reagent; clinical trial monitoring; cosmetic; nutriceutical; mutation detection; gene expression analysis; transgenic animal; nochropic; cytostatic; antiinflammatory; single nucleotide polymorphism; SNP; gene therapy; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymucleotides encoding human lipases that are structurally related to animal lipases, particularly phospholipase B, useful for drug screening, diagnosis and in gene therapy of biological disorders.
                                                                                                                   388
                             ELASI YOGOGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQR
                                                              EDFAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNNMLEPVGRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Ala raplaces Val in a polymorphic variant
(ABB09555)"
                                                                                                                                                                                                                                                                                                                             TVVWRCRRGGRREDPPMSLRTVAL 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NHL (Val 1318 variant).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB09556 standard; protein; 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-2002; 2002WO-US001715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-2001; 2001US-0264049P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miranda M, Turner CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lipase
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Yu X,

1254

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1074

ABB09556;

148

1014

33

Gaps

32;

Length 1458; Indels 956 INLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVM 1015

ELASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQR 1016 ELASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQR EDFAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNNMLEPVGRKT 1076 EDFAVVVQPPFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNNMLEPVGRKT 389 TSNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLYWAVPVAAGVGLVVGIIG

269

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329

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209 INLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVM

896 LETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPD 149 LETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPD

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955

1135

448

388

328

1136 TSNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLYWAVPVAAGVGLVVGIIG 1195

TVVWRCRRGGRREDPPMSLRT 1216

1196 449

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TVVWRCRRGGRREDPPMSLRT 469

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ABU65083 standard; protein; 1423 AA

ABU65083 ID ABU6

RESULT

NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer; hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;

Human NOV24c protein.

20-MAY-2003

ABU65083;

us-09-778-961-2.rag

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The present invention relates to novel human phospholipase-like enzymes and polynucleotides encoding such proteins. Sequences of the invention care useful for producing a medicament for modulating the activity of phospholipase in a disease such as cancer, inflammation, cardiovascular chaspease in a disease such as cancer, inflammation, cardiovascular disease, demortia disease, demortia disease, perkinson's disease, corticobasal degeneration, charbeimer's disease, Perkinson's disease, corticobasal degeneration, cardo mentia, schizophrenia with dementia, Korsakoff's psychosis, pain associated with CNS (e.g. epilepsy, failed back surgery syndrome, callergic disease including asthma, allergic rhinitis (hay fever), acopic dematitis, anaphylaxis and inflammation, cardiovascular disease, chronic dematitis, anaphylaxis and inflammation, cardiovascular disease, chronic constructive pulmonary disease, acute respiratory distress syndrome, gout, cattery disease, emphysema or obesity. They are also used for treating anorexia, overweight, cachexia, bullmia, hypertension, type-II diabetes, coronary artery disease, hyperlipidaemia, gall bladder disease, ostecarthritis, artery disease, hyperlipidaemia, gall bladder disease, ostecarthritis, colon cancer), thrombolytic disease, reduced fertility, polycystic colon cancer), thrombolytic disease, reduced fertility, polycystic charact hyperlipidaemia, shiperson, menstrual irregularity, human when heaven heaven.
anaphylaxis; inflammation; acute respiratory distress syndrome; diabetes;
                 chronic obstructive pulmonary disease; emphysema; obesity; anorexia; overweight; cachexia; bulimia; hypertension; coronary artery disease; type-II diabetes; hyperlipidaemia; gall bladder disease; osteoarthritis; gout; sleep apnoea; respiratory problem; polycystic ovarian syndrome; thrombolytic disease; reduced fertility; pregnancy; stress incontinence; hirsutism; menstrual irregularity; depression; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human phospholipase-like enzyme polypeptide useful for screening agents, and in the treatment of cancer, inflammation, diabetes, obesity, a central nervous system disorder, or a cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; Fig 2; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human phospholipase like enzyme
                                                                                                                                                                                                                                                                                                                                  09-OCT-2001; 2001WO-EP011641.
                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2000; 2000US-0238445P.
26-DEC-2000; 2000US-0257293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-426287/45.
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                                                                                                                                                                                                                                  WO200231161-A2
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2001US-0274322P.
2001US-0274849P.
2001US-0275235P.
2001US-0275578P.
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2001US-0275601P
2001US-027600P
2001US-0276776P
2001US-027679P
2001US-0276299P
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2001US-0277327P.
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2001US-0278894P.
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2001US-0280233F.
2001US-0280802F.
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                                                                                                                 WO200272757-A2.
                                                                                                 Homo sapiens.
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-MAR-2001;
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20-MAR-2001;
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02-APR-2001;
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                                                                                                                                    19-SEP-2002
                                                                               human.
EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDGN 148
                                                                                                                                                                                                                                                                                                                                                                                 716 MRELVGSGRYDTQEDFSVVIQPPFQNIQLPVLADGLPDTSFFAPDCIHPNQKFHSQLARA 775
                                                                                                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                                                                                                                1 MRELVGSGRYDTQEDFSVVLQPFFQNIQLPVLA------33
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                                                            98.1%; Score 2469; DB 5; Length 1216; 93.0%; Pred. No. 1.4e-226; ive 2; Mismatches 1; Indels 32.
                                                                                                                                                                                                                                                                               Conservative
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466;

Matches

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1043

148

EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDGN

33 ----ALEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT

MRELVGSGRYDTQEDFSVVLQPFFQNIQLPVL

g à 원 LETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSP-

149 1104

83

ò g 8 MELASLY QQQGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQ

1164

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DINLEKOWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEV

207

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This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABU65218 represent the NOVX polypeptides encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
), Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
M, Gangolli E, Vernet CAM, Guo X, Tchernev V;
R, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
Catterfor E, Burgess C, Leite M, Zhong H, Alsobrook JP;
Kieger DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOVX polypeptides and polymucleotides, useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 170; 1103pp; English.
                      04 APR-2001; 2001US-0281194P.
13-APR-2001; 2001US-0283675P.
30-APR-2001; 2001US-028367424P.
02-MAY-2001; 2001US-0288342P.
03-MAY-2001; 2001US-0288342P.
15-MAY-2001; 2001US-02883P.
15-MAY-2001; 2001US-0291190P.
16-MAY-2001; 2001US-0291190P.
16-MAY-2001; 2001US-0291190P.
30-MAY-2001; 2001US-0291190P.
31-MAY-2001; 2001US-0291485P.
31-MAY-2001; 2001US-0294889P.
31-MAY-2001; 2001US-0299027P.
18-UNN-2001; 2001US-0299027P.
                                                                                                                                                                                                                                             2001US-0309198P.
2001US-0312903P.
2001US-0318470P.
2001US-0325430P.
2001US-0325681P.
2001US-0330390P.
2001US-033331P.
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2002US-0345705P.
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2001US-0304354P.
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N-PSDB; ABX97050.
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Fernandes ER,
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10-SEP-2001;
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Zerhusen BD,
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GTVVWRCRRGGRREDPPMSLRTVAL 472

1399

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447

REDFAVVVOPPFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWINMLEPVGRK 387

TISNNFTHSRAKIKCPSPESPYLYTIRNSRILPPDQAEEAPEVLYWAVPVAAGVGLVVGII

1219

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267

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cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; antiniertility; cardiomypathy; atherosclerosis; hypotension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease; parkinson's disease; asthma; fertility disorder; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; vaccine.
                 Ä
                ADH42431 standard; protein; 1423
                                                                                                                                                                                                                                                                                                                 2002US-0385615P.
2002US-0385755P.
2002US-0386041P.
2002US-038635P.
2002US-038643PP.
2002US-038645P.
2002US-0386465P.
                                                                                                                                                                                                                                                                              04-JUN-2003; 2003WO-US017573.
                                                                                                                                                                                                                                                                                                      2002US-0385490P
                                                                                       Novel human protein NOV65d
                                                                (first entry)
                                                                                                                                                                                                                                    WO2003102159-A2
                                                                                                                                                                                                                                                                                                        04-JUN-2002;
04-JUN-2002;
04-JUN-2002;
05-JUN-2002;
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06-JUN-2002;
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                                            ADH42431;
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           ADH42431
RESULT
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4

Gaps

38;

95.6%; Score 2407; DB 5; Length 1423; ilarity 91.5%; Pred. No. 1.6e-220; Conservative 1; Mismatches 4; Indels 38.

Query Match Best Local Similarity Matches 462; Conserv

Sequence 1423 AA;

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2002US-0387696P-
2002US-038769P-
2002US-038760P-
2002US-0388022P-
2002US-0388432P-
2002US-0388132P-
2002US-0389120P-
2002US-0389146P-
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15-AUG-2002; 2
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ä Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda E, Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;
Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller E, Malyankar UM, Returajan M, Peyman JA, Qian X, Rastelli L;
Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;
Wolenc AR, Zhong M, Zhong H;

WPI; 2004-053467/05. N-PSDB; ADH42430.

New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, in chromosome mapping, tissue typing or in pharmacogenomics.

Claim 2; SEQ ID NO 984; 1503pp; English.

The invention relates to 566 new isolated human polypeptides and their

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1220 MELASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQ 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences comprising one or more conservative substitutions in these. The polypeptide, polynucleotide and antibodies against the polypeptides are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This sequence represents an example of the polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148
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 genes, sequences that are at least 95% identical to these or
                                                                                                                                                                                                                                                                                                                                                                                ----ALEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT
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08-MAR-2001; 2001US-0274191P.
08-MAR-2001; 2001US-0274194P.
08-MAR-2001; 2001US-0274281P.
09-MAR-2001; 2001US-0274849P.
09-MAR-2001; 2001US-0275835P.
13-MAR-2001; 2001US-0275579P.
13-MAR-2001; 2001US-0275579P.
13-MAR-2001; 2001US-0275579P.
14-MAR-2001; 2001US-0275579P.
15-MAR-2001; 2001US-0275601P.
16-MAR-2001; 2001US-027670P.
16-MAR-2001; 2001US-027670P.
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10-SEP-2001;
12-SEP-2001;
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27-SEP-2001;
18-OCT-2001;
31-OCT-2001;
14-NOV-2001;
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28-MAR-2001;
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TCHERNEY V T. FERNANDES E R. CASMAN S J. MALYANKAR U M. GERLACH V.

(GUOX/) (TCHE/) (FERN/) (CASM/) (MALY/) (GERL/) (/XDIT) ANDE/)

PATTURAJAN M. GANGOLLI E A. VERNET C A M.

(GORM/) (MILL/) (KEKU/) (PATT/)

GUO X S.

VERN/)

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ZERHUSEN B

GUSEV V Y. GORMAN L. MILLER C F KEKUDA R.

(LILL/) (ZERH/) (GUSE/) (JIWW/)

ALSOBROOK J P.

LEPLEY D M. RIEGER D K. BURGESS C E.

(ALSO/) (ALSO/) (LEPL/) (RIEG/) (BURG/)

CATTERTON E. LEITE M W. ZHONG H.

(SPAD/) (CATT/) (LEIT/)

ANDERSON D W. SPADERNA S K.

The invention relates to an isolated polypoptide (designated NOVX, or NOV1-NOV127) comprising a sequence selected from 178 fully defined amino acid sequences (and their mature forms, variants and fragments). Also acid sequences (and their mature forms, variants and fragments). Also cincluded are an isolated nucleic acid molecule encoding Novx, a vector comprising the nucleic acid, a cell comprising the vector, methods for comprising the presence or amount of the polypeptide or the nucleic acid molecule in a sample, methods for determining the presence of expression of the above polypeptide or nucleic acid molecule in a first mammalian of the above polypeptide or nucleic acid molecule in a first mammalian of the above polypeptide or nucleic acid molecule in a first mammalian of subject, a method for identifying an agent that binds to the above subject, a method for identifying an agent that binds to the above cuse in the treatment of a pathology that is related to aberrant or a modulator of a modulations of the polypeptide and a method for identifying a ctivity or of latency or predisposition to a pathology associated with the polypeptide and a method for modulating consequence in the treatment of a modulation of a pathology associated with the polypeptide and a method for modulating consequence, obesity, infectious diseases, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or pathoneous mapping, tissue typing, preventive medicine and achoremacogenomics. The polypeptides are also useful as vaccines. The present sequence represents a NoVX protein of the invention. New NOVX polypeptides and nucleic acid molecules useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or Li, R, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li Gusev VY, Ji W, Gorman L, Miller CE, Kekuda R; Gangolli BA, Verriet CAM, Guo XS, Tchernev VT; Casman SJ, Malyankar UW, Gerlach V, Liu Y; Spaderna SK, Catterton E, Leite MW, Zhong H; Lepley DM, Rieger DK, Burgess CE; Claim 1; SEQ ID NO 86; 786pp; English. Spytek KA, Gusev VY, WPI; 2004-225693/21. N-PSDB; ADN61816. pharmacogenomics Padigaru M, Sp Zerhusen BD, G Patturajan M, Fernandes ER, Anderson DW, S Alsobrook JP,

Sequence 1423 AA;

PADIGARU M. SPYTEK K A. SHENOY S G. TAUPIER R J. PENA C E A.

(PADI/) E (SPYT/) E (SHEN/) E (TAUP/) T (PENA/) E

Score 2387; DB 8; Length 1423; Pred. No. 1.3e-218; 94.8%; 91.1%; Query Match Best Local Similarity

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                                                             EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDCN 148
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                                                                                      LETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSP- 207
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                   MELASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQ
                                     ----LEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT
                                                                                                                DINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEV
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1; Mismatches
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PR 15-WAY 2010 2001US-0313146P
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Zerhusen BD, Gusev V, Ji W, Gorman L, Miler CE, Kekuda R;
Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;
Pernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;
Lepley DM, Rieger DK;

WPI; 2002-723332/78. N-PSDB; ABX97048.

NOVX polypeptides and polynucleotides, useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma.

Claim 1; Page 168-169; 1103pp; English.

This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive

Query Match Best Local

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Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL; Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR; Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L; Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR; Malachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE; Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L; Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
                                                                    04 JUN - 2002; 2002US - 0385615P.
04 JUN - 2002; 2002US - 0385755P.
05 JUN - 2002; 2002US - 0386355P.
06 JUN - 2002; 2002US - 0386355P.
06 JUN - 2002; 2002US - 0386357P.
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06 JUN - 2002; 2002US - 0386459P.
07 JUN - 2002; 2002US - 0386465P.
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2002US-0406182P.
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2002US-0423748P
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                        04-JUN-2003; 2003WO-US017573
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12-JUN-2002;
12-JUN-2002;
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11-JUN-2002; 2
11-JUN-2002;
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11-DEC-2003
 cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; noctropic; antiparkinsonian; antiasthmatic; antiinfertility; cardiomypathy; atherosclerosis; hypotrension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease; Parkinson's disease; asthma; fertility disorder; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MELASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQ 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               267
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                                                                                                                                                                                                                                                                                                                                                                                                   149 LETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARA-RDMPAQAWDLVERNKNSP 207
                                                                                                                                                                                                                                               921 MRELVGSGRYDTQEDFSVVLQPFFQNIQLPVLQDGLPDTSFFAPDCIHPNQKFHSQLARA 980
                                             e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine, ABUG5041-ABUG5218 represent the NOVX polypeptides encoded by
                                                                                                                                                                                                                     32
                                                                                                                                                                                                                                                                                88
 activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEV
                                                                                                                                                                                                                                                                                ----ALEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT
                                                                                                                                                                                         Gaps
                                                                                                                                                                                         39;
                                                                                                                                                         5; Length 1419;
                                                                                                                                                                                         8; Indels
                                                                                                                                                                           .2e-214;
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                                                                                                                                                             92.8%; Score 2336.5;
89.1%; Pred. No. 9.2e
:ive 8; Mismatches
                                                                                                                                                                                                                        1 MRELVGSGRYDTQEDFSVVLQPFFQNIQLPVL-
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                                                                                                                                                                                                Matches 450; Conservative
                                                                                                                                                                                 Similarity
                                                                                                      ABX97008-ABX97185
                                                                                                                                   Sequence 1419 AA;
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RESULT 10 ADH42427

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                           01-JUL-2004
                                                                                                                                                                                    04-MAR-2004
   ADN61813;
   The invention relates to 566 new isolated human polypeptides and their encoding genes, sequences that are at least 95% identical to these or sequences comprising one or more conservative substitutions in these. The polypeptide, polymucleotide and antibodies against the polypeptides are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, Parkinson's disease, asthma, or fertility disorders. Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The example of the polypeptide of the invention.
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                                                                     New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
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 Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ; Zhong H;
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89.1%; Pred. No. 9.2e-214;
cive 8; Mismatches 8; Indels 39;
                                                                                                                                  Claim 2; SEQ ID NO 980; 1503pp; English
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Matches 450; Conservative
Spytek KA, Stone DJ,
Wolenc AR, Zhong M,
                                    WPI; 2004-053467/05
                                                                                                           pharmacogenomics.
                                              N-PSDB; ADH42426
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DX O1-UUL-2004 (first entry)

XX Human novel protein NOV24a.

XW Human, NOVX, diabetes; obesity; infectious disease; anorexia; cancer sensoised cachesia; according disease.

XX Human, NOVX, diabetes; obesity; infectious disease.

XX Human, NOVX, diabetes; infectious d
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composition and methods

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14-NOV-2001; 2001US-0333722P.
21-NOV-2001; 2001US-0332094P.
03-DEC-2001; 2001US-033746FP.
04-DEC-2001; 2001US-0338092P.
04-DEC-2001; 2001US-033185P.
03-JAN-2002; 2002US-0345705P.
2001US-0332272P.
2001US-0333184P.
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Gusev VY,
                                                                                                                                                     FERNANDES E R.
CASMAN S J.
MALYANKAR U M.
                                                                                                                        PATTURAJAN M.
GANGOLLI E A.
VERNET C A M.
GUO X S.
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                                                                                                                                                                                  ANDERSON D W. SPADERNA S K.
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RIEGER D K.
BURGESS C E.
                                                   PADIGARU M.
SPYTEK K A.
SHENOY S G.
TAUPIER R J.
PENA C E A.
                                                                                                       GORMAN L.
MILLER C E.
KEKUDA R.
                                                                                       ZERHUSEN B D.
                                                                                                                                                                                               CATTERTON E.
                                                                                                                                                                                                    LEITE M W.
ZHONG H.
                                                                                                                                                                       GERLACH V.
                                                                                             GUSEV V Y.
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Zerhusen BD, G.
Patturajan M, Fernandes ER, Anderson DW, S.
      14-NOV-2001;
14-NOV-2001;
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(LEPL/)
(RIEG/)
(BURG/)
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(GERL/)
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Shenoy SG, Taupier RJ, Pena CEA, Li L Ji W, Gorman L, Miller CE, Kekuda R; EA, Vernet CAM, Guo KS, Tchernev VT; Malyandar UW, Gerlach V, Liu Y; K, Catterton E, Leite MW, Zhong H; Rieger DK, Burgess CE; Gusev VY, Ji W, Gorman L, Gangolli EA, Vernet CAM, Caman SJ, Malyankar UM, Spaderna SK, Catterton E, I Lepley DM, Rieger DK, Burs, Alsobrook JP,

WPI; 2004-225693/21. N-PSDB; ADN61812

New NOVX polypeptides and nucleic acid molecules useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; SEQ ID NO 82; 786pp; English.

The invention relates to an isolated polypeptide (designated NOVX, or NOVI-NOVI27) comprising a sequence selected from 178 fully defined amino NOVI-NOVI27) comprising a sequence selected from 178 fully defined amino acid sequences (and their mature forms, variants and fragments). Also included are an isolated nucleic acid molecule encoding NOVX, a vector comprising the nucleic acid, a call comprising the vector, methods for comprising the presence of amount of the polypeptide or the nucleic acid determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian of the above polypeptide or identifying an agent that binds to the above polypeptide, a method for identifying a potential therapeutic agent for polypeptide, a method for identifying a potential therapeutic agent for use in the treatment of a pathology that is related to aberrant capturession or physiological interactions of the polypeptide, a method of screening for a medulator of activity or of latency or predisposition to screening to a pathology associated with the polypeptide and a method for modulating

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lipid-associated molecule, LIPAM, neuroprotective; relaxant; antithyroid, antidiabetic; cytostatic; dermatological; immunosuppressive; antidiabetic; cytostatic; dermatological; immunosuppressive; antidialamatory; thyromimetic; antialergic; cerebroprotective; gastrointestinal; hepatotropic; anticonvulsant; yartipacterial; antiparabitic; fungicide; protozoacide; virucide, uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV; nootropic; LIPAM agonist; LIPAM antagonist; gene therapy; neurodegenerative disorder; parkinson's disease; Alzheimer's disease; muscular disorder; myotonic dystrophy; catatonia; endocrine disorder; grave's disease; cancers;
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the activity of the polypeptide cited above. The composition and method are useful for diagnosing, preventing or treating diseases such as diabetes, obesity, infectious diseases, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders like Alzheimer's disease, parkinson's disease, immune disorders, haematopoietic disorders, dyslipidaemias, and other chronic diseases. These may also be used in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The polypeptides are also useful as vaccines. The present sequence represents a NOVX protein of the invention.
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                                                                                                                                                                                                                                                                                                                              33 ----ALEPIGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT
                                                                                                                                                                                                                                                                                                                                                                                             EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDGN
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                                                                                                                                                                                                  DB 8; Length 1419;
                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                 Score 2336.5; DB 8;
Pred. No. 9.2e-214;
8; Mismatches 8;
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                                                                                                                                                                                                      92.8%;
ilarity 89.1%;
Conservative
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Best Local Similarity
                                                                                                                                                                            Sequence 1419 AA;
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955 MRELVGSGRYDTQEDFSVVLQPFFQNIQLPVLADGLPDTSFFAPDCIHPNQKFHSQLARA 1014

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This invention relates to novel human lipid-associated molecules (LIPAM)
and the DNA sequences which encode them. The invention may be useful for
the production of compounds with a neuroprotective, relaxant,
antithyroid, antidabetic, cytostatic, dermatological, immunosuppressive,
antinflammatory, thyromimetic, antiallergic, cerebroprotective,
cantinflammatory, thyromimetic, antiallergic, cerebroprotective,
cantinflammatory, thyromimetic, antiallergic, cerebroprotective,
antiparkinsonian, antibacterial, antiallergic, fungicide, protozoacide,
cyllocide, uropathic, antirheumatic, cardiant, cardiovascular, anti-HIV or
contropic activity acting as LIPAM agonists or antagonists. In addition,
the disclosed sequences may be useful for gene therapy. The invention may
contropic activity acting as LIPAM agonists or antagonists. In addition,
the disclosed sequences may be useful for gene therapy. The invention may
contropic activity acting as LIPAM, agonists or addition,
the disclosed sequences may be useful for general addition,
the abnormal expression or activity of LIPAM, such as
with an abnormal expression or activity of LIPAM, such as
confocular disorders (for example Parkinson's disease), cancers (for
example leukaemia, cervical or breast cancers), immunological disorders
(for example scleroderma, systemic lupus erythematosus, allergies),
casample allergic and sorders (for example Crohn's disease), renal disorders
(for example Goodpasture's syndrome), infections (for example
casample doodpasture's syndrome), infections
cirrhosis). LIPAM or its fragments may also be used in screening for
compounds that specifically bind to and modulate the activity of LIPAM.
The polynucleotides can be used to create humanised animals or transgenic
compounds
condel human disease. The present sequence is that of a human
continued that present example of the invention.
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Kable AE, Khare R;
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immunological disorder; scleroderma; systemic lupus erythematosus; allergy; gastrointestinal disorder; Crohn's disease; renal disorder; Goodpasture's syndrome; infection; viral; bacterial; fungal; parasitic; protozoal; helminthic; cardiovascular disorder; atherosclerosis; hepatic disease; cirrhosis; transgenic animal; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gietzen KJ, Hafalia AJA, Jackson AA, K
uis JP, Murage J, Swarnakar A, Yang YG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 10; 207pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 2002US-0426105P.
; 2002US-043315P.
; 2003US-045312TP.
; 2003US-0454801P.
; 2003US-0465495P.
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24-APR-2003; 2003US-0465619P
01-AUG-2003; 2003US-0491800P.
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                                                                                                                                                                                                                               Homo sapiens
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1314
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              1015 LWTNMLEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT
                                                        1075 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDGN
                                                                                                    INLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVM
                                                                                                                                                                                       ELASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQR
                                                                                                                                209 INLEKDWKLVTLPIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVM
                                                                                                                                                                          269 ELASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQR
                                                                                                                                                                                                                    EDFAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNMLEPVGRKT
                                                                                                                                                                                                                                EDFAVVVQPPFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNNM------
                                                                                                                                                                                                                                                               389 TSNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLYWAVPVAAGVGLVVGIIG
                                             EWKASNSVPTSVHQLRPAD1KVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWS1GGDGN
                                                                                      LETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPD
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1421. .1443 /label= transmembrane_binding_domain
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714. 1059
/label= repeat_region_3
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/label= signal_peptide
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/label= rep
367. .712
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MRELVGSGRYDTQEDFSVVLQPFFQNIQLPVLA

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57;

Indels

Length 1433;

DB 8;

92.7%; Score 2334.5; DB 8; 88.7%; Pred. No. 1.5e-213; ive 0; Mismatches 0;

Best Local Similarity 88.7 Matches 447; Conservative

Query Match

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TTSNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLYWAVPVAAGVGLVVGII 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELASLYQQQGGKÇAM-LAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQ 327
                                                                      - useful as
                                                                                                                           The present sequence is a protein which has both phospholipase B and lipase activity. The claimed protein comprises at least amino acids 367-712 of this sequence. The phospholipase is useful as a supplement to pancreatic phospholipase and as a reagent for the determination of
                                                                                                                                                                                                                                                                                                                                                             EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDGN
                                                                                                                                                                                                                                                                                                                              ---ALEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                        Length 1450;
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                                                                        B and lipase activity
                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                        68.1%; Score 1715.5; DB 2; 66.9%; Pred. No. 3.4e-154; ive 53; Mismatches 76;
                                                                                                                                                                                                                                                                       1 MRELVGSGRYDTQEDFSVVLQPFFQNIQLPVL-
                                                                         DNA encoding protein with phospholipase supplement to pancreatic phospholipase.
                                                                                                            Claim 1; Page 7-12; 16pp; Japanese.
                                                                                                                                                                                                                                           Best Local Similarity 66.9
Matches 327; Conservative
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                                         WPI; 1997-520744/48
         (TOJO/) TOJO H.
(TOFU ) TONEN CORP.
                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                       Sequence 1450 AA;
                                                     N-PSDB; AAT91874
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Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;

Human protein sequence SEQ ID NO:1339

(first entry)

16-OCT-2001 AAM25824;

AAM25824 standard; protein; 267 AA.

AAM25824

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AAM55965 The proteins can have activities based on the tissues and cells can have activities based on the tissues and cells they are expressed in, such as antiinflammatic; they are expressed in, such as antiinflammatic; antiantheuric; immunosuppressive; antibacterial; endocrine; cardiovascular; antianaemic; antianaemic antianaemi
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          anti-HTV; fungicide; antimutagen; cardiovascular; antianaemic; anti-HTV; fungicide; antimutagen; cardiovascular; antianaemic; antiangregant; haemostatic; valnezary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antiagpressant; nootropic; antiparkinsonian; infection; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; antianaphylactic; neuropathology; cardiac antiphylactic; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; althma; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 DF---SVVIQPFFQN-IQLPV--LALEPIGSKTETLDLRAEMPITCFTQNEPFLRTPRNS
central nervous system; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human polymucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
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92.3%; Pred. No. 1.6e-104;
ive 4; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-2000; 2000WO-US035017.
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                                                                                                                                                                                                                                                                                                   neurological disorder
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differentiation activities; stem cell growth factor activity;

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SSDLPTSWRGLSWSIGGDGNLFTHTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGAR 188
                                                                    Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                                                                                                                                                                                          haematopoiesis regulation; tissue growth; immunomodulator; activing inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastassis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atheroselerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; cissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antinflammatory; antiarthritic; haemostatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                     ARDMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQ
                            SSDLPTSWRGLSWSIGGDGNLETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGAR
                                                                                                                                                                                                                                                                                                   Human phospholipase B homologue, SEQ ID NO:1423.
                                                                                                                                                                                                                ABB11053 standard; peptide; 267 AA.
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27-APR-2000; 2000US-00560875.
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nes 228; Conservative
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell

Claim 20; Page 140; 1963pp; English.

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Sequence 21, Appl Sequence 166, Appl Sequence 166, Appl Sequence 166, Appl Sequence 166, Appl Sequence 161, Appl Sequence 1781, Appl Sequence 28, Appl Sequence 279, Appl Sequence 279, Appl Sequence 279, Appl Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli

Sequence 1 Sequence 1 Sequence 2

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Sequence:

Minimum DB Maximum DB

Database

Result No.

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208 DINLEKDWKLVTLFIGVNDLC-HYCENPEAHLATE-YVQHIQQALDILSEELPRAFVNVV 265
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US-09-270-767-59726
Sequence 59726, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPRENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 59726
: LENGTH: 107
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REPERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62577
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 44304
LENGTH: 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.4%; Score 336.5; DB 4; Length 215; 41.7%; Pred. No. 5.8e-28; tive 29; Mismatches 71; Indels 5;
US-09-134-000C-3943

US-08-96-101-166

US-08-08-92-54-166

US-09-124-698-166

US-09-124-598-166

US-09-124-523-166

US-09-124-523-166

US-09-10-279-50

US-09-710-279-50

US-09-710-279-50

US-09-710-279-1528

US-09-107-5328-352-7177

US-09-107-5328-5799

US-09-107-5328-5799

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US-09-323-878-29
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; ORGANISM: Drosophila melanogaster
US-09-270-767-44304
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Best Local Similarity 41.7%
Matches 75; Conservative
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    TYPE: PRT
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

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                 version 5.1.6 - 2005 Compugen Ltd
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US-09-248-76A-14950
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US-09-621-855-2
US-09-800-170-3
US-09-800-170-3
US-09-336-115C-14
US-09-336-115C-14
US-09-189-129-2
US-09-189-128-2
US-09-189-128-2
US-09-328-35-4
US-09-328-35-5
US-09-338-115C-2
US-09-338-115C-2
US-09-338-115C-2
US-09-338-115C-2
US-09-338-115C-2
US-09-900-256-5
US-09-949-016-11382
US-09-949-016-11383
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                                                                                                                                                                                                                                                                                                                                                                     513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993
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length: 2000000000
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2518
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Perfect score:
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307 GELQCIGATTLDEYRKNIEKDAALERRRQPVQVDEPSVVDTVAILKGLRD-----RYEA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 VVAGTKYRGBFEÉRLKKVMEBIQQAGNVILFIDELHTLVGAGGAEGAIDASNILKÞALAR 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 ADIKUVAALGD---SLTTAVGARPNNSSDLPTSWRGLSWSIGGDGNLE----THTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 PNILK---KENPYLLGFSTSTWEGTAGLNVAAEG-ARA------RDMPAQAWDL--
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4000 Bell Atlantic Tower, 1717 Arch Stre
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Best Local Similarity 21.6%; Pred. No. 0
Matches 97; Conservative 51; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NLEKDWKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,843
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER: 60/057,535
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAWE: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10082
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GM10082
                                                        Sequence 2, Application US/09040843
Patent No. 6124119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----VERMKN----
                                                                                                                     Jaworski, Deborah J.
                                                                                                                                                                                                                                                                                                                                                                                                          STATE: PA
COUNTRY: USA
ZIP: 19103-2793
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: IBM Compatible
Windows
                                                                                                                                                                                                Fosberry, Andrew
Hodgson, John E.
Lawlor, Elizabeth
                                                                                                                                                                                                                                                            Rosenberg, Martin
Ward, Judith
                                                                                                                                       Wang, Min
Shilling, Lisa K.
Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 866 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MecB
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                Philadelphia
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                                                                                                  GENERAL INFORMATION:
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STREET: 400
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APPLICANT:
APPLICANT:
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APPLICANT:
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                             RESULT 4
JS-09-040-843-2
                                                                                                                                                                  APPLICANT
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: VUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
FILE REFERENCE: 107196.132
FILE REPERENCE: 107196.132
FRICH APPLICATION NUMBER: US 60/074,725
FRICH APPLICATION NUMBER: US 60/074,725
FRICH APPLICATION NUMBER: US 60/096,409
FRICH FILING DATE: 1998-02-13
FRICH FILING DATE: 1998-02-13
FRICH FILING DATE: 1998-08-13
FRICH FILING DATE: 1998-08-13
FRICH FILING DATE: 1998-02-13
FRICH FILING DATE: 1998-02-13
FRICH FILING DATE: 1998-02-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- EMAIALWINNILE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 DMPAQAW-----DLVERMKNSPDINLEKDWKLVT--LFIGVNDLCHY-----CEN-- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 CTEWKASNSVPISVHOLRPADI-----KVVAALGDSLTTAVGARPNNSSDLPTSWRG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 LSWSIGG----DGNLETHTILPNILKKF----NPYLLGFSTSTWEGTAGLNVAAEGARAR 190
                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 LGSKTETLDLRAEMPITCPIQNEPFLR-----TPRNSNYTYPIKPA---IENWGSDFL 86
                                                                                                                             168 GFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDL 227
                                                                                                                                                      234 -----PEAHLATEYVQHIQQ-ALDILSEELPRAFVNVVEVMELASLYQGQGGKCAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----BINS-----
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 20.2%; Pred. No. 0.036;
Matches 94; Conservative 54; Mismatches 138; Indels 179;
                                                                                           5;
                                                      DB 4; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 PVGRKITSNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEBAP 427
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                                                                                              Indels
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                                                                                                                                                                                                              228 C-HYCENPEAHLATE-YVQHIQQALDILSEELPRAFVNVV 265
                                                                                                                                                                                                                                          635 QVTQYYGTSSSISDTSIVGNİQDPVIPVLSEDL--TFTILLE-
                                                      6.4%; Score 160.5; DB 4;
38.0%; Pred. No. 2.7e-09;
tive 18; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :::|::::::|
479 ASQDRVSDSEPCFSAACRTASMCLDLFGGGKIISLL-
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                                                                                                                                                                                                                                                                                                                                                    Sequence 14950, Application US/09248796A
Patent No. 6747137
, ORGANISM: Drosophila melanogaster
US-09-270-767-59726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I FTHYRAMNEFGHNRAK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Candida albicans
US-09-248-796A-14950
                                                                6.4
Best Local Similarity 38.0
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                           RESULT 3
US-09-248-796A-14950
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--SPDI-- 209
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                                                                                                                                                                                                                                                                           307 GELQCIGATTLDEYRKNIEKDAALERRFQPVQVDEPSVVDTVAILKGLRD-----RYEA 360
                                                                                                                                                                                                                                                                                                                                            180 LNVAAEGARARDMPAQAWDLVER----MKNSPDINLEKDWKLVTLFIGVNDLCHYCENPE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --AHLATEYVQHIQQALDILSEELPRAFVNVV------EVMELASLYQGQGGK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 CAMILAAQNNCTCLRHSQSSIE-KQELKKVNWN----LQHGISSFSYWHQYTQREDFAVVV 335
    ---THTTL 155
                                                                                                                                                                                                                                                                                                                   H-----NVVEVMELA 271
                                                                                                                                                                                                                                                                                                                                                                                               SLYQGQGGKCAMLAAQ--NNCTCLRHSQSSLEKQ-ELKKVNW-NLQHGISSFSYWHQYTQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                   419 EIEKVKNEKDAAVHAQEFENAANLRDKOTKLEKOYEEAKNEWKNAONGMST----SLS 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REDFAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNNMLEPVGRK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 RFANDVSRIALHAGTISTIQLEAAPSNLYDTIIGLPVEVNTTLWRVIINQSSFYSYSTDK 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPFFQNTLTP---LNERGDIDLTFFSEDCFHFSDRGHAEMAIALWNNMLEP-VGRKTISN 391
                                215 INPEDNGALNKYLPDWVWELSSQQCKILLNSLCLG-----NCLFTKNDDTLHYFSTSE
                                                                                 156 PNILK---KFNPYLLGFSTSTWEGTAGLNVAAEG-ARA------RDMPAQAWDL--
                                                                                                                                                                                                                                        ---VTLFIGVNDLCHYCENPEA
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    106 ADIKVVAALGD---SLTTAVGARPNNSSDLPTSWRGLSWSIGGDGNLE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kinsella, Todd
APPLICANT: Kinsella, Todd
TITLE OF INVENTION: 1N VIVO PRODUCTION OF CYCLIC PEPTIDES
FILE REFERENCE: A-66614-1/DJB/RNG/RNK
CURRENT APPLICATION NUMBER: US/09/800,170
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/187,130
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.9%; Score 98.5; DB 4;
19.9%; Pred. No. 0.21;
ative 43; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 TTSNNFT----HSRAKLKCPS-PESPYLY 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              515 DAVNSISKAVRRARAGLKDPKRPIGSFIF 543
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                                                                                                                                                              ---VERMKN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.9%
Best Local Similarity 19.9%
Matches 53; Conservative
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                    SLYQGQGGKCAMLAAQ--NNCTCLRHSQSSLEKQ-ELKKVNW-NLQHGISSFSYWHQYTQ 327
                                                                                                         419 EIEKVKNEKDAAVHAQEFENAANLRDKÖTKLEKÖYEEAKNEWKNAQNGMST----SLS 472
                                                                                                                                                      REDFAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNNMLEPVGRK 387
                                                                                                                                                                               ---LATEYVOH---IQOALDILSEELPRAFV-----NVVEVMELA 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.0%; Score 100; DB 3; Length 866;
21.6%; Pred. No. 0.45;
.ive 51; Mismatches 119; Indels 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                  388 TISNNFT----HSRAKLKCPS-PESPYLY 411
                                                                                                                                                                                                                                                                      515 DAVNSISKAVRRARAGLKDPKRPIGSFIF 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/621,855
FILING DATE: 24-Jul-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10082
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/040,843
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jaworski, Deborah J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burnham, Martin
Fosberry, Andrew
Hodgson, John E.
Lawlor, Elizabeth
Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09621855
Patent No. 6346608
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 215-994-2488
TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Min
Shilling, Lisa K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 866 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVENTION: MecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Meck
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 21.64
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: <Unknown>
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237
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APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAFEUTICS FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 GVISPL--KALNYLIHQFDSDİVTVDYRVRGFTRDİEGRKHFID--HEINSİ---QNYLS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TQREDFAV--- 333
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                                                                                                                                                                                                                                                     --VNWNLQHGISSFSYWHQYTQREDFAVVVQPFFQNTLT---PLNERGDTDLTFFSEDCF 362
                                                                                                                                                                                                                                                                                                                                                                                                                                        ---FTHSRAKLKCPSPE 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 YLSS-NHLNGSIPSWIFSLPSLVELDLSNNTFSGKIQEFKSKTLSAVTLKQNKLKGRIPN 447
                                                                                                                                      307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 AGLNVAAEG-----ARARDMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 PVGRK-----TISNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVL 430
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                                                                                                         --AHLATEYVOHIQOALDILSEELPRAFVN
                                                                                                                                                                                                                                                                                                                                                              342 SLVNNNFDGGLEFLSF-NTQLERLDLS-----SNSLTGEIPSNISGLQNL----ECL
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                                | | | : : | | | : : : | | | : : : | | | | : : : | | | | : : : | | | : : | : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | : | | : : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                  264 VVEVMELASLYQGQGGKCAM-----LAAQNNCTCLRHSQSSLEK-----QELKK-
---DWKLVTLFIGVNDL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 24.7%; Pred. No. 0.11;
Matches 73; Conservative 39; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 QNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PELICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27435
     184 AEGARARDMPAQAWDLVERMKNSPDINLEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                363 HFSDRGHAEMAIALWNNMLEPVGRKTTSNN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27435, Application US/09252991A patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                       -----CHYCENPE-
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S--LLNQKNLQLL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 SPYLYTLRNSRLL 419
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US-09-252-991A-27435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSWDGVHCDETT-GQVIALDLRCSQLQGKFHSNSSLFQLSNLKRLDLSFNNFTGSLISPK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GLNVA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 LDLRAEMPITCPTQ-----NEPFLRTPRNSNYTYPIK------PAIENWGSDFLC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LALSSSLPHLCPEDQALSLLQFKNMFTINPNASDYCYDIRTYVDIQSYPRTLSWNKSTSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                               Sequence 2, Application US/08666271
; Sequence 2, Application US/08666271
; Patent No. 592000
; GENERAL INFORMATION:
APPLICANT: JONES, JONATHAN D
APPLICANT: THOMAS, COLWYN M
APPLICANT: THOMAS, DAVID A
; APPLICANT: JONES, DAVID A
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, BTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 169;
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19.9%; Pred. No. 0.66;
Live 59; Mismatches 167; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION COMPATIBLE
COMPUTER: FLORDY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPANIOS SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,271
FILING DATE: 19-SEP-1996
CLASSIFICATION DATA:
PRILICATION DATA:
PRESIDENCY NUMBER: PCT/GB94/02812
RILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
PRILING DATE: 23-DEC-1994
PRIOR APPLICATION NUMBER: GB 9326428.1
PILING DATE: 24-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GGDGNLETHTTLPNILKKFNPYLLGFSTSTWEGTA-----
                                   392 NFTHSRAKLKCPSPESPYLYTLRNSR 417
                                                                         | : : : : : | : | 426 RFVYYKGPVYCLTGPNNVFYVQRNGK 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: GB 9326428.1 FILING DATE: 24-DEC-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9409363.0 FILING DATE: 11-MAY-1994 ATTORNEY/ARRY INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REGISTRATION NUMBER: 620-7
TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 863 amino acids
amino acid
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Best Local Similarity 19.9
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ropology:
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                                                                                                                                                                                     RESULT 7
US-08-666-271-2
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---AAEGARARDMPAQAWDLVERMK----NSP---- 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 SESSGAATTWAPSWQTAGGGKNSCATFGAEFSAASDMINNAQKIVQETQQLSANQPKNIT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 ---DINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LAQKMLKNAQSQAEILK-----LANQ 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 VEVMELASLYOGQ----GGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNW-----NLQHG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 ALGDSLTTAV-GARPNNSSDLPTSWRGLSWSIGGDGNLETHTTLPNILKKFNPYLLGFST 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 ISSFSYWHQYTQREDFAVVVQPFFQNTLTP-LNERGDTDLTFFSEDCFHFSDRGHAEMAI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                3.9%; Score 97.5; DB 4; Length 640;
20.8%; Pred. No. 0.5;
ive 49; Mismatches 123; Indels 129; Gaps
           Sequence 14, Application US/09336115C

Patent No. 657634

GENERAL INFORMATION:
APPLICANT: Weltzin, Richard A.
APPLICANT: Guy, Bruno
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Wethods Against Helicobacter Infection
TITLE OF INVENTION: UNMBER: US/09/336,115C
CURRENT APPLICATION NUMBER: US 09/100,258
FRIOR APPLICATION NUMBER: US 09/100,258

PRIOR FILING DATE: 1998-06-19
NUMBER: OF SEQ ID NOS: 24

SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Burkly, Linda C
APPLICANT: Benjamin, Christopher D
APPLICANT: Benjamin, Christopher D
APPLICANT: Heasion, Catherine A
APPLICANT: Whitty, Adrian
TILLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 LSSLK----TSAADF-----NNQTPQINQAQNLANTLIQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 NSNYTYPIKPAIENWGSDFLCTEWKASNSVPTSVHQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 ALWINMLEPVG--RKTTSNN 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                442 -LGNNPFRNMGMIASSTINN 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09189129
Patent No. 6323027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 OPHNLNLNTPSSLTA-----
                                                                                                                                                                                                                                                                                                                                    ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.99

Query Match
Best Local Similarity 20.89
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STWEGTAGLNV---
                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(21)
US-09-336-115C-14
                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SIGNAL
US-09-336-115C-14
                                                                                                                                                                                                                                                                                               LENGTH: 640
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-09-189-129-2
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114 LGDSLTTAVGARPNNSSD-----LPTSWRGLSWSIGGDGNLETHTTLPNILKKFNP 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 NDLCHYC--ENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVMELASLYQGGGGKCA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 MLAAQNNCTCLRHSQSSLEKQELKKVNWN-----LQHGISSFSYW-HQYTQ----RE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 KFSLPSVDGQKRYMFRVRSR-----FNPLC-----GSAQH----WSEWSHPIHWGSN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 TTSNNFTHSRAKLKCPSPE----SPYLY-----TLRNSR-----LLPDQAEEAPEVL 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 YLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 EEITSGCOLOKKEIHLYQTFVVOLODPRE-----PRR--QATOMLKLONL-----V 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 DFAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNNMLEPV--GRK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 KGVGLNTTI-LTPNGNEDTTADFFLTTMPTD----SLSV-----STLPLPEVQCFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 94.5; DB 3; Length 482;
Pred. No. 0.64;
2; Mismatches 133; Indels 125; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431 Y-WAVPVAAGVGLVVGIIGTVVWRCRRGGRREDPPMSLRTVAL 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 FNWYVD------GVEVHNAKTKPREEOYNSTYRVVSV 340
       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,129
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         CIP
                                                                                                                                                                                                                                                                                                                                                                NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199
REFENCE/DOCKET NUMBER: 34,199
RELEPROCE/DOCKET NUMBER: 4006 PCT CI:
TELEPHONE: 617 679-2000
TELEPAC: 617 679-2038
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Burkly, Linda C
Benjamin, Christopher
                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: A006 PCT CIP
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 60/017,466
FILING DATE: 10-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.8%; Sur
20.6%; Pred
62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 20.0.
Best Local 83; Conservative
ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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25;

Hession, Catherine A

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/057,535
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                             Sequence 4, Application US/09040843
Patent No. 6124119
                                                                                                                                                                                   Jaworski, Deborah J.
                                                                                                                                                                                                                                                                                                                                                        Hodgson, John E.
Lawlor, Elizabeth
                                                                                                                                                                                                                         Wang, Min
Shilling, Lisa K.
                                                                                                                                                                                                                                                                                                                     Fosberry, Andrew
Hodgson, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 672 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                     Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: PA
COUNTY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-040-843-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 MLAAQNNCTCLRHSQSSLEKQELKKVNWN------LQHGISSFSYW-HQYTQ-----RB 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 IPWAPENLTLHKLSESQLE-----LNWNNRFLNHCLEHLVQYRTDWDHSWTEQSVDYRH 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 DFAVVVQPPFQNTLTPLNERGDTDLTPFSEDCFHFSDRGHAEMAIALMNNMLEPV--GRK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 KFSLPSVDGQKRYMFRVRSR-----FNPLC-----GSAQH----WSEWSHPIHWGSN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 EEITSGCQLQKKEIHLYQTFVVQLQDPRE-----PRR--QATQMLKLQUL-----V 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 LGDSLTTAVGARPNNSSD------LPTSWRGLSWSIGGDGNLETHTTLPNILKKFNP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 YLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 FNVEYMACTW-----NSSSE-PQPTNLTLHYW-----YKNSDNDKVQK-----CSHYLFS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 NDLCHYC--ENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVMELASLYQGQGGKCA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGVGLNTTI-LTPNGNEDTTADFFLTTMPTD----SLSV-----STLPLPEVQCFV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.8%; Score 94.5; DB 4; Length 482; Best Local Similarity 20.6%; Pred. No. 0.64; Matches 83; Conservative 62; Mismatches 133; Indels 125;
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM POTA:

APPLICATION NUMBER: US/09/824,286

FILING DATE: 10-AAY-1996

APPLICATION NUMBER: 60/017,466

FILING DATE: INFORMATION:

NAME: KAPLAN, WATER: 4,199

REFERENCE/DOCKET NUMBER: 34,199

REFERENCE/DOCKET NUMBER: 34,199

REFERENCE/DOCKET NUMBER: A006 PCT CIP

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:

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TELECOMUNICATION INFORMATION:

TELECOMPUTER: A006 PCT CIP

TELECOMUNICATION INFORMATION:

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TELECOMUNI
Whitty, Adrian
TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
NUMBER OF SEQUENCES: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y-WAVPVAAGVGLVVGIIGTVVWRCRRGGRREDPPMSLRTVAL 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-824-286-2
                                                                                                                                            ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 482 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                               CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         COUNTRY: USA
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18; 261 FVNVVEVMELASLYQCQGGKCAMLAAQ--NNCTCLRHSQSSLEKQ-ELKKVNW-NLQHGI 316 116 DSLTTAVGA----RPNNSSDL--PTSWRGLSWSIGGD-----GNLETHTTLPNILKKFN 163 164 PY-----RDWPAQAWDLV 200 190 PVQVDEPSVVDTVAILKGLRDRYEAHHRINISDEAIEÀAVKLSNRYVSDRFLPPKAIDĽI 249 201 ERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRA 260 250 D--EASSKVRL------ 280 -----KDAAVHAQEFENAANLRDKQTKLEKQYEEAKNEWKNAQNGM 321 Ouery Match
3.8%; Score 94.5; DB 3; Length 672;
Best Local Similarity 21.8%; Pred. No. 1.1;
Matches 74; Conservative 44; Mismatches 103; Indels 119; Gaps APPLICANT: Rosenberg, Martin
APPLICANT: Ward, Judith
TITLE OF INVENTION: MecB
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre SOFTWARE: FABLISEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,843

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ERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRA 260
                                                                                                                        261 FVNVVEVMELASLYQGQGGKCAMLAAQ--NNCTCLRHSQSSLEKQ-ELKKVNW-NLQHGI 316
                                                                                                                                                                                ----KDAAVHAOEFENAANI, RDKOTKI, EKOYEEAKNEWKNAONGM 321
                                                                                                                                                                                                                                           317 SSFSYWHQYTQREDFAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIAL 376
                                                                                                                                                                                                                                                                                |: | | : | | : 322 ST-----SLSEEDIAEVIAGWTGIPLTXINE---TE----SEKLLSLEDTLHERV---
                                           ----TYPIKPAIENWGSDFLCTEWKASNSVPTSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                         ::: | | | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::
                                                                                                                                                                                                                                                                                                                                                                 377 WNNMLEPVGRKTTSNNFT----HSRAKLKCPS-PESPYLY 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.7%; Score 94;
20.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 7914, Application US/09328352; Patent No. 6562958; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i ORGANISM: Acinetobacter baumannii
US-09-328-352-7914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 20.6 hes 85; Conservative
                                                                 D--EASSKVRL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-328-352-7914
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                                                                 250
      201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 PY-----RLGFSTSTWEGTAGLNVAAEGARA------RDMPAQAWDLV 200
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21.8%; Pred. No. 1.1;
ive 44; Mismatches 103; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: BM Compatible
COMPUTER: BM Compatible
COPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/621,855
FILING DATE: 24-011-2000
CLASSIFICATION SATA:
APPLICATION DATA:
PRIOR APPLICATION WINBER: 09/040,843
FILING DATE: <UNKNOWN-
FILING DATE: <UNKNOWN-
ATTORNEY/AGENT, INFORMATION:
                                                                                                                                                       377 WNNMLEPVGRKTTSNNFT----HSRAKLKCPS-PESPYLY 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10082
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jaworski, Deborah J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fosberry, Andrew
Hodgson, John E.
Lawlor, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosenberg, Martin
Ward, Judith
OF INVENTION: MecB
OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09621855
Patent No. 6346608
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 215-994-2488
TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang, Min
Shilling, Lisa K.
Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 672 amino acids
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity Zicco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <Unknown>
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                                                                                                                                                                                                                                                                                                   US-09-621-855-4
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317
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APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 IFGSHÖNOKFD----ACFDGLLIANGAR---SQLRPKAWVKVDKAYPWGAAWSIVP--- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 LETHTTLPNILKKF---NPYLLG------FSTSTWE-GTAGLNVAAEGARAR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -ECOVLDSEILHQFYDRSKIMMGILPTGAIPTEPQQRLSSVFWSLPTPQLQSFLQDEQAK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 DMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQAL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----QAW-LKQVSERWPKV---ADW------LKEILYNSQTQPKWLSANY-----R 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DILSEELPRAFVNVV-EVMELASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 DVVMTQFGQGRIGVIGDAAHAMSPQLGQGANMALLDAWAFSQSLQHAQKN-----QNID 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 LVNSHYREASTNLYGLGIHRATLCHVLTQKLSEYSSQI---TWCMNHSVESFVEHNDEVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VGSGRYDTQEDFSVVLQPFFQNIQLPVLALEPLGSKTETLDLRAEMPITCPTQNEPFLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 VGAG-----LLLQP-----AGLAVFEHLGVLDKALTLGAK--VTGLEGQLPDKRL
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US-09-336-115C-2
US-09-336-115C-2
, Sequence 2, Application US/09336115C
, Patent No. 6576244
, GENERAL INFORMATION:
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247 QQALDILS-----EELPRAFVNVVEVMELASLYQGQGGK------- 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 PADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIG------GDGNLE 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.7%; Score 94; DB 4; Length 708;
Best Local Similarity 18.9%; Pred. No. 1.4;
Matches 77; Conservative 56; Mismatches 137; Indels 138; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 NTLIPLNERGDIDLIFFSEDCFHFSDRGHAEMAIALMNNMLEPVGRKT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Guy, Bruno
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILER REFERENCE: 06132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT APPLICATION NUMBER: US/09/100,258
PRIOR FILING DATE: 1999-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 708
                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Helicobacter pylori
APPLICANT: Weltzin, Richard A.
                                                                                                                                                                                                                                                                                     , NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-336-115C-2
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Search completed: March 25, 2005, 14:38:13 Job time: 54 secs

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March 25, 2005, 14:36:30 ; Search time 144 Seconds (without alignments) 1085.275 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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2518
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Perfect score:
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Maximum DB &
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	Sequence 1, Appli	86,		Sequence 1423, Ap	Sequence 1339, Ap	Sequence 9, Appli	Sequence 7025, Ap	Sequence 5575, Ap	Sequence 1728, Ap	Sequence 4078, Ap	Sequence 2029, Ap	Sequence 84, Appl
	ΩI	US-10-054-691-2	US-10-478-245-1	US-10-092-900A-86	US-10-092-900A-82	US-10-276-774-1423	US-10-296-115-1339	US-10-478-245-9	US-10-369-493-7025	US-10-369-493-5575	US-10-264-237-1728	US-09-764-891-4078	US-10-094-749-2029	US-10-092-900A-84
		13		15							15		15	15
	Query Match Length DB	1458	1458	1423	1419	267	267	696	382	414	101	148	270	310
de	Query	99.0	99.0	92.6							20.9		18.5	18.1
	Score	2492	2492	2407	2336.5	1185	1185	884.5	599.5	551.5	527	527	465.5	456.5
	Result No.	1	7	٣	4	ហ	9	7	œ	6	10	11	12	13

		Sequence 13312, A Sequence 178287,		Sequence 178758,	Sequence 157323,	1609,	192	e 517	Sequence 5586, Ap	Sequence 12424, A	Sequence 12789, A	Sequence 44278, A	Sequence 8573, Ap					830	Seguence 8574, Ap	Sequence 28, Appl	Sequence 14, Appl	Sequence 58899, A	Sequence 3296, Ap		Sequence 47664, A	
Sn	US-10-369-493-5161 US-10-276-774-1607	3 5	85		US-10-437-963-1573				US-09-815-242-5586	US-09-815-242-12424	US-09-815-242-12789		US-10-335-977-8573								US-08-834-666A-14		US-10-104-047-3296			US-10-437-963-166059
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981 348 349	132	069	462	773	1063	1027	1028	646	810	818	818	818	426	458	.839	1004	1010	1460	524	633	640	641	791	417	472	3662
16.4 16.1 13.4	13.1 9.3	4.2	4.4	4 .1	4.1	4.0	4.0	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9		3.9	3.9	3.8	3.8
414 406.5 336.5	329	106	102.5	102	102	99.5	99.5	66	66	66	66	66	98.5	98.5	98.5	98.2	98.5	98.5	97.5	97.5	97.5	97.5	97.5	97		96.5
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ALIGNMENTS

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Sequence 2, Application US/10054691

Publication No. US20020115846A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wiranda, Maricar
APPLICANT: Wiranda, Maricar
APPLICANT: Wiranda, Maricar
APPLICANT: Wiranda, Maricar
APPLICANT: Wiranda, Maricar
TITLE OF INVENTION: O. US20020115846A1e1 Human Lipase and Polynucleotides Encoding t
FILE REFERENCE: LEX-0303-USA
CURRENT APPLICATION NUMBER: US/10/054,691

CURRENT PILING DATE: 2001-01-22

PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1015 LWTNMLEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT 1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- 33
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Pred. No. 1.2e-226;
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Best Local Similarity 93.7%;
Matches 472; Conservative
                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-054-691-2
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Best Local Similarity
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OTHER INFORMATION: Incyte ID No: 2440624CD1
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US-10-478-245-1
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                                                                                                                            INLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVM 268
                                                                                                                                                                                                               ELASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQR
                                                                                                                                                                                                                                                                                               EDPAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMA.IALWNNMLEPVGRKT
                                                   149 LETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPD
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YAO, Monique G.; ARVIZU, Chandra S.;
LU, Yan; GANDHI, Ameena R.;
GRIFFIN, Jannifer A.; ELLIOTT, Vicki S.;
LU, Dyung Aina M.; LEE, Ernestine A.;
LEE, Soo Y.; YUE, Huibin;
YANG, Junming; TRIBOULEY, Catherine M.;
KABLE, Amy E.; SWARNAKAR, Anita
INVENTION: LIPID-ASSOCIATED MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YUE, Henry; AZIMZAI, Yalda;
BAUGHN, Mariah R.; BURFORD, Neil;
REDDY, Roopa; CHAWLA, Narinder K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFRENCES: PI-0427 USA
CURRENT APPLICATION NUMBER: US/10/478,245
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: PCT/US02/15688
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2001-05-18
PRIOR PLICATION NUMBER: US 60/292,242
PRIOR PLILING DATE: 2001-05-18
PRIOR PLILING DATE: 2001-05-25
PRIOR PLILING DATE: 2001-05-25
PRIOR PLILING DATE: 2001-06-01
PRIOR PLILING DATE: 2001-06-01
PRIOR PLILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/303,404
PRIOR APPLICATION NUMBER: US 60/314,754
PRIOR PLILING DATE: 2001-08-24
PRIOR PLILING DATE: 2001-08-24
PRIOR PLILING DATE: 2001-08-24
PRIOR PLILING DATE: 2002-01-22
PRIOR PLLING DATE: 2002-01-22
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Publication No. US20040171009A1
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NAME/KEY: misc_feature
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NUMBER OF SEQ ID NOS:
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1375 TSNNFTHSRAKLKCPSPESPYLYTLRNSKLLPDQAEEAPEVLYWAVPVAAGVGLVVGIIG 1434
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                                                                                                                                                                                                                                                                                                                         209 INLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVM 268
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                                                                                                                                                   149 LETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPD
                                                                                                                              34 -----LEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPALENWGSDFLCT
                                  Gaps
                                32;
 Length 1458;
                                  Indels
Score 2492; DB 16;
Pred. No. 1.2e-226;
0; Mismatches 0;
                                                                  1 MRELVGSGRYDTQEDFSVVLQPFFQNIQLPVLA-----
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Shenoy, Suresh G.
Taupler Jr., Raymond J.
Pena, Carol E.A.
Li, Li
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ernandes, Elma R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Charles E.
Ramesh
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     99.0%;
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Gerlach, Valerie
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Vernet, Corine A
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erhusen, Bryan
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Ji, Weizhen
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      Query Match
Best Local Similarity 93.77
Matches 472; Conservative
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Spaderna,
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Kekuda,
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APPLICANT:
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APPLICANT: Alsobrook, John P.
APPLICANT: Alsobrook, John P.
APPLICANT: Alsobrook, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Rieger, Daniel K.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION NO US20040043382Alel Proteins and Nucleic Acids Encoding Same FILE OF INVENTION NUMBER: US/10/092, 900A
CURRENT APPLICATION NUMBER: US/10/092, 900A
CURRENT FILING DATE: 2001-03-08
PRIOR PELICATION NUMBER: USSN 60/274,322
PRIOR APPLICATION NUMBER: USSN 60/274,281
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
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1339 TTSNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLYWAVPVAAGVGLVVGII 1398
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                                                                                                         1399 GTVVWRCRRGGRREDPPMSLRTVAL 1423
                                                                    GTVVWRCRRGGRREDPPMSLRTVAL
                                                                                                                                                                                                                                                                            US-10-092-900A-82
; Sequence 82, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Padigaru, Muralidhara APPLICANT: Spytek, Kimberly A. APPLICANT: Shenoy, Suresh G. APPLICANT: Taupier Jr., Raymond APPLICANT: Pena, Carol E.A. APPLICANT: Li, Li
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Gangolli, Esha A.
Vernet, Corine A.M.
Goo, Xiaojia Sasha
Tchernev, Velizar Fernandes, Elma R.
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Zerhusen, Bryan D.
Gusev, Vladimir Y.
Ji, Weizhen
Gorman, Linda
Miller, Charles E.
Kekuda, Ramesh
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Catterton, Elina
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Malyankar, Uriel
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Gerlach, Valerie
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Zhong, Haihong
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ORGANISM: Homo sapiens
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APPLICANT: ALOSDOK, John P.
APPLICANT: Rieger, Daniel K.
APPLICANT: Rieger, Daniel K.
APPLICANT: Rieger, Daniel K.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION No. US20040043382Alel Proteins and Nucleic Acids Encoding Same FILE REPERRNCE: 21402-290C
CURRENT FILING DATE: 2002-03-07
CURRENT FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR PLILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: USSN 60/274,281
PRIOR PLILING DATE: 2001-03-08
PRIOR PLILING DATE: 2001-03-08
PRIOR PLILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR PLILING DATE: 2001-03-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRELVGSGRYDTQEDFSVVLQPFFQNIQLPVL
                             Leite, Mario W.
Zhong, Haihong
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US-10-092-900A-86
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LENGTH: 1423
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GENERAL INFORMATION:
APPLICANT: NUCYTE CORPORATION; TANG, Y. Tom;
APPLICANT: YUE, Henry; AZIMCAL, Yalda;
APPLICANT: BAUGHN, Mariah R.; BURFORD, Neil;
APPLICANT: REDDY, Roopa; CHAWLA, Narinder K.;
                                                                                                                                                                                                                                              ; Sequence 1339, Application US/10296115; Publication No. US20040053248A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT , ORGANISM: Homo sapiens US-10-296-115-1339
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261 ALDILSE 267
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US-10-296-115-1339
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US-10-478-245-9
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                                                                                                                                            388 TISNNETHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLYWAVPVAAGVGLVVGII 447
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APPLICANT: Hyeeq, Inc.
APPLICANT: Hyeeq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2000-11-18
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 1433
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                                                                                                                             33 ----ALEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT
                                                                                                                                                                               EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDGN
                                                                                                                                                                                                                                               39; Gaps
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                        Score 2336.5; DB 15; Length 1419;
Pred. No. 6.9e-212;
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                                                   8; Indels
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Similarity 92.3%; Pred. No. 1.2e-103;
28; Conservative 4; Mismatches 9;
                                                                              1 MRELVGSGRYDTQEDFSVVLQPFFQNIQLPVL------
                       92.8%; Scor.
89.1%; Pred. No. o...
8; Mismatches
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                                   92.8
Best Local Similarity 89.1
Matches 450; Conservative
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US-10-276-774-1423
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          JS-10-092-900A-82
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Best Local Si
Matches 228;
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TITLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
FILE REPERENCE: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT: 784PCT:
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                                                                                                                                                                                                 189 ARDMPAQAMDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVOHIOO
81 NYTYPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNN
                                                                                                                                       129 SSDLPTSWRGLSWSIGGDGNLETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGAR
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47.1%; Score 1185; DB 15;
Best Local Similarity 92.3%; Pred. No. 1.2e-103;
Matches 228; Conservative 4; Mismatches 9;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Glater, Steven C.
APPLICANT: Glater, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Glater, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7025
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianteng
APPLICANT: Chen, Xianteng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 KASNSVPTSVHQLRPADIKVVAALGDSLT-----TAVGARPNNSSDLPTSWRGLSWS 142
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      : | :: : | |: | |: | 683 HKF-ENKINITCPNQVQPFLRTYKNSMQGHGTWLPCR-DRAFSALH 726
                                                                                                                                                    US-10-369-493-7025
Sequence 7025, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Caenorhabditis elegans US-10-369-493-7025
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                        APPLICANT: YAO, Monique G ; ARVIZU, Chandra S.;
APPLICANT: LU, Yan; GANDHI, Amena R.;
APPLICANT: GRIFFIN, Jennifer A.; ELLIOTT, Vicki S.;
APPLICANT: RAMKUMAR, Jayalaxmi; LAL, Preeti G.;
APPLICANT: LU, Dyung Aina M.; LEB, Ernestine A.;
APPLICANT: LEE, Soo Y.; YUE, Huibin;
APPLICANT: YANG, Junming; TRIBOULEY, Catherine M.;
APPLICANT: YANG, Junming; TRIBOULEY, Catherine M.;
APPLICANT: KABLE, Amy B.; SWARNAKAR, Anita
TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
FILE REFERENCE: PI-0427 USN
Debopriya; NGUYEN, Danniel B.;
Monique G.; ARVIZU, Chandra S.;
                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 10.047 USX
CURRENT FILING DATE: 2003-11-18
PRIOR PULING DATE: 2003-11-18
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-18
PRIOR PILING DATE: 2001-05-25
PRIOR PLING DATE: 2001-05-25
PRIOR PAPLICATION NUMBER: US 60/293,726
PRIOR PILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/295,346
PRIOR PILING DATE: 2001-06-01
PRIOR PILING DATE: 2001-06-01
PRIOR PILING DATE: 2001-06-01
PRIOR PILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/314,754
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/368,799
PRIOR PILING DATE: 2002-01-22
PRIOR PILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/368,799
PRIOR PILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 20
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; OTHER INFORMATION: Incyte ID No: 7504684CD1
US-10-478-245-9
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61 WAVPVAAGVGLVVGIIGTVVWRCRRGGRREDPPMSLRTGAL 101

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94 NSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRG-LSWSIGGDGNL-ET 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 LEPLGSKTETLDLKAEMPITCPTQNEPFLKTPRNSNYTYPIKPAIENWGSDFLCTEWKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 LEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCTEWKAS
                                                                                                                                                                                                                                                                                                                                                                                                        Length 148;
                                                                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
FULE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER: OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4078
                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

20.9%; Score 527; DB 10;
Best Local Similarity 78.3%; Pred. No. 1.4e-41;
Matches 108; Conservative 9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION MASCHALL ABOUNT ABPLICATION MASCHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
TITLE OF TOWNEY OF 1084355/0160
CURRENT APPLICATION WHEBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION WHERE: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR PILING DATE: 2001-09-14
NUMBER: OF SEQ ID NOS: 3381
SOUTHARE: PATENTIN OF: 3381
SOUTHARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2029, Application US/10094749
Publication No. US20030219741A1
                                                                 Sequence 4078, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 HHTAOHSEEVOPLPPWLL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTTLPNI -- LKKFNPYLL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WAKAVATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAMECHIKA, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Homo sapiens
US-09-764-891-4078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-10-094-749-2029
                                          RESULT 11
US-09-764-891-4078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 VVQPFFQNTL-TPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALMNNMLEPYGRKTTSNN 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                     193 PAQAMDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENP-----EAHLATEYVOHIQ 247
                                                                                                                                                                                                                                                                                                                                                                                                           141 IGQARALVNTWHAHSEINVKEDWKLVNIFIGANDICVYCEDPYFNSTALHGNATFEKNII 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 IDKKKYFCEGLHT-FECDC--ESNKQFTDDDIQGVCFGYMNAEKDIQNTGLFDNKDDFTF 317
                                                                                                                                                                                                                                                                                                                                 GLSWSIGGDGNLETHTILPNILKKFNPYLLGF----STSTWEGTAGLNVAAEGARARDM 192
                                                                                                                                                                                                                                                     24 NWSCD--ASVMAKSKKVPTSAHSVRFADIKVIGALGDSLTAANGAGAQAGADPLAVILQYR 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAIALWINNLEPVGRKTTSNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 QALDIISEELP-----RAFVNVVEVMELASLYO
                                                                                                                                                                                                                             80 NWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTA--VGARPNNSSDLPTSWR
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                                                                                                                                                                                            53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 527; DB 15; Length 101;
Pred. No. 7.8e-42;
); Mismatches 1; Indels (
                                                                                                                                                      DB 15; Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          432 WAVEVAAGVGLVVGIIGTVVWRCRRGGRREDPPMSLRTVAL 472
                                                                                                                                                                                              Indels
                                                                                                                                                   Query Match
21.9%; Score 551.5; DB 15;
Best Local Similarity 34.4%; Pred. No. 3.3e-43;
Matches 132; Conservative 56; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1728, Application US/10264237

Sequence 1728, Application US/00649181

GENERAL INFORMATION:
Publication No. US2004000949181

STILE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFRERCE: PA131P1

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR FILING DATE: 2001-05-18

PRIOR FILING DATE: 2001-05-18

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2876

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: Patentin Ver. 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 LSDPSVGLHCPSTNCPFFPTTKNS 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                              TYPE: PRT Caenorhabditis elegans US-10-369-493-5575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.9%;
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Best Local Similarity 99.0
Matches 100; Conservative
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Homo sapiens
US-10-264-237-1728
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US-10-264-237-1728
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LENGTH: 101
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                                                                   LENGTH:
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US-10-369-493-5416

Sequence 5416, Application US/10369493

Sequence 5416, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Color, Yonger

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-10 (52052)

CURRENT APPLICANTON NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICANTON NUMBER: US 60/360,039

PRIOR PRILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 NVVEVME---LASLYQGQGGKCAMLAAQNNCTC-LRHSQSSLEKQELKKVNWNLQHGISS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 FSYWHOYTOREDFAVVVOPFFONTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWN 378
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                 FRIOR PULICATION NUMBER: USSN 60/238,092

PRIOR APPLICATION NUMBER: USSN 60/274,281

PRIOR APPLICATION NUMBER: USSN 60/274,281

PRIOR APPLICATION NUMBER: USSN 60/274,191

PRIOR PETLING DATE: 2001-03-08

PRIOR PETLING DATE: 2001-03-08

PRIOR PETLING DATE: 2001-03-30

PRIOR PETLING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: USSN 60/304,354

PRIOR PETLING DATE: 2001-07-10

PRIOR PETLING DATE: 2001-07-33

PRIOR PETLING DATE: 2001-07-33

PRIOR FILING DATE: 2001-05-31

PRIOR FILING DATE: 2001-05-31

PRIOR FILING DATE: 2001-05-31

PRIOR FILING DATE: 2001-06-31

PRIOR PETLING DATE: 2001-06-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 MKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
18.1%; Score 456.5; DB 15; Length 310;
Best Local Similarity 41.6%; Pred. No. 2.2e-34;
Matches 99; Conservative 38; Mismatches 90; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Caenorhabditis elegans
US-10-369-493-5416
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Best Local Similarity 29.89
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-092-900A-84
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TILE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                              61 NLVTVLEIVNLRELYQEKKVYCPRMILRSLCPCVLKFDDNSTELATLIEFNKKFQEKTHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                     203 MKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFV 262
                                                                                                                                                                                                                                                                                        263 NVVEVME---LASLYQGQGGKCAMLAAQNNCTC-LRHSQSSLEKQELKKVNWNLQHGISS 318
                                                                                                                                                                                                                                                                                                                                                                                     319 FSYWHQYTQREDFAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWN 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 IMLEPVGRKTTSINNFTHSRAKLKCPSPESPYLYTLRNS-----RLLLPDQAEEAPEVLY-- 431
                                                                                                                                                                                                                       Gaps
                                                                                                                                              23;
                                                                                                 DB 15; Length 270;
                                                                                            18.5%; Score 465.5; DB 15; Length 39.9%; Pred. No. 2.5e-35; tive 39; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432 ------WAVPVAAGVGLVVGIIG-TVVW 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 SVHALRPADIQVVAÁLGDSLTVRTLGPQVVW 269
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FILING DATE: 2001-03-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 84, Application US/10092900A Publication No. US20040043382A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Padigaru, Muralidhara
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Pena, Carol E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gorman, Linda
Miller, Charles E.
Kekuda, Ramesh
Patturajan, Meera
Gangolli, Esha A.
Vernet, Corine A.M.
Guo, Xiaojia Sasha
Tchernev, Velizar T.
Fernandes, Elma R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spaderna, Steven K.
Catterton, Elina
Leite, Mario W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhong, Haihong
Alsobrook, John P.
Lepley, Denise M.
Rieger, Daniel K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malyankar, Uriel M.
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zerhusen, Bryan D.
Gusev, Vladimir Y.
Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Casman, Stacie J.
                                                                                                                     Best Local Similarity 39.99
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 21402-2900
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2029
                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-092-900A-84
                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
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356 FFSEDCFHFSDRGHAEMALALMNNMLEPVGRKTTSNNFTHSRAKLKCPSPESPYLYTLRN
                                                                                                                                               Search completed: March 25, 2005, 14:49:39
Job time : 152 secs
                                                                                                        346 SKM 348
                                                                            416 SRL 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 LEKQELKKVNWNLQHGISSFSYWHQYTQR---EDFAVVVQPF-FQNTLTPLNERGDIDLT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 RIVENOKKLD-DLSDGYRNVSYDFQNNEHFNSNDFTVVVQPFATEYTDSYRDEHGKYNPT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAEGARARDMPAQAMDLVERMKNSPDINLEKDWKLVTLFIGVND---LCHYCENPEAHLA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 TEXVQHIQQALDII.SEELPRAFVNVVEVMELASLYQGQGGKCAMLAAQNNCTCLRHSQSS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 NSSDLPTSWRGLSWSIGGDGNLETHTTLPNILK----KFNPYLLGFSTSTWEG-TAGLNV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 IKPAIENWGSDFLCTEWKASNSV-----PTSVHQLRPADIKVVAALGDSLTTAVGARPN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 NIVGQRQRYPGNAFFTGMDFEVDRHLTVYNIFRIIABKTGNKLFGGSTGIDYGENTGLNV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                 231 IMPPINVKIHSQAHKLSKFCEFSHRKTCSCI-FELNEKEYQNIKKQFDEQLNEVVEQFN- 288
                                                                                                                                                                    264 VVEVMELASLYQGQG-GKCAMLAAQNNCTCLRHSQSSLEKQELKK-VNWNLQHGISSFSY 321
                                                                                                                                                                                                                                                                         322 WHQYTQREDFAVYVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAENAIALMNNML 381
                                                                                                       263
                    DFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSI 143
                                                                                    203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 VÄMALE-------KYLNSIDPHEIYPDDVNMIKPHHIRVIGAMGDSLT--IGSRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47; Gaps
                                                                                                                                                                                                                                                                                                                                                            144 GGDGNLETHTILPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERM
                                                                                                                                                 204 KUSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATBYVQHIQQALDILSEELPRAFVN
                                                                                                                                                                                                                                                                                                                                          382 EPVGRKTISNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLYWAVPVA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 16.1%; Score 406.5; DB 15; Length 348; Best Local Similarity 32.2%; Pred. No. 1.5e-29; Matches 117; Conservative 66; Mismatches 133; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 6523, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Caenorhabditis elegans US-10-369-493-6523
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-10-369-493-6523
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM protein - protein search, using sw model	Run on: March 25, 2005, 14:27:20 ; Search time 47 Seconds (without alignments) 966.262 Million cell updates/sec
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	(*ILLIDOL ALLYMETER) 966.262 Million cell updates/s	8/88
Title: Perfect score:	US-09-778-961-2 2518	
Sequence:	1 MRELVGSGRYDTQEDFSVVLACRRGGRREDPPMSLRTVAL 472	472

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	1933.5	76.8	1458	~	A45665	adult-specific bru
7	599.5	23.8	382	~	T20655	hypothetical prote
e	551.5	21.9	414	7	T26083	
4	414	16.4	981	~	T16060	
S	406.5	16.1	348	7	T24016	
9	336.5	13.4	349	7	T24015	_
7	329	13.1	425	~	T21835	hypothetical prote
80	101	4.2	ო	~	T38084	0
σ	101	4.0	٣	7	875251	hypothetical prote
10	99.2	4.0	480	7	JC7672	
11	99.5	4.0		~	C87618	excinuclease ABC,
12	66	3.9		7	F89819	endopeptidase [imp
13	66	3.9	913	~	T15278	hypothetical prote
14	66	3.9	1804	~	T34518	nestin - golden ha
15	98.5	3.9	863	~	A55173	cf-9 protein precu
16	98.5	3.9	1010	~	T09499	ATP-dependent clp
17	97.5	ō.	524	7	E71881	hypothetical prote
18	97.5		641	7	A64667	outer membrane pro
19	97	9. 9.	575	Н	VCLJHD	env polyprotein pr
20	96	3.8		~	AE2051	endopeptidase Clp
21	9	3.8	1498	~	B97355	DNA segregation AT
22	95.5	3.8		~	T45619	hypothetical prote
23	95	3.8	362	~	A24710	
24		3.8	390	~	T07246	hypothetical prote
25	95	3.8	583	~	E75529	u
56	95	3.8	734	~	837998	probable serine/th
27	94.5	3.8	571	0	T29643	hypothetical prote
28	94	3.7	708	~	H64631	outer membrane pro
29	94	3.7	1014	~	832613	HEX2 protein - yea

LIM domain protein hypothetical prote	protein kinase xaz probable two compo	auxin-regulated prorobable adenosine	cyclin A - bovine	beta-tubulin cofac	quinolinate synthe	succinate-CoA liga	hypothetical prote	retinoblastoma bin	conserved hypothet	hypothetical prote	outer membrane pro	protein-tyrosine-p
T40395 AD3190	T10725 A81806	T00515 T30869	S24788	T47885	F87609	S74793	AE2357	138902	A69939	S45886	C71840	A49724
0 0	~ ~	~ ~	7	7	~	~	~	ч	~	7	~	н
1150	996 505	595	406	1249	377	401	742	1721	255	552	703	1118
3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.6	3.6	3.6	3.6
93.5	93.5 93	6 6 6	92.5	92.5	92	92	92	92	91.5	91.5	91.5	91.5
30	33	3.4 3.5	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT A45665 adult- C;Spec C;Date C;Date C;Acce R;Bocc R;Bio	T 1 -specific cies: Ory e: 03-May ession: A 1, W.; Scl ol. Chem.	A45665 adult-specific brush border esterase/phospholipase (EC 3) precursor - rabbit C;Specific brush border esterase/phospholipase (EC 3) precursor - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004 C;Accession: A45665 E;Accession: A45665 B;Boll, W.; Schmid-Chanda, T.; Semenza, G.; Mantei, N. J;Boll, Chem. 268, 12901-12911, 1993 A;Title: Messenger RNAs expressed in intestine of adult but not baby rabbits. Isolation
A,Ref A,Acc A,Mol A,Res A,Cro C,Key	A;Reference number: A A;Accession: A45665 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1458 cB A;Cross-references: U C;Keywords: hydrolase	A;Reference number: A45665; MUID:93286138; PMID:8509424 A;Accession: A45665 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1458 <bol> A;Cross-references: UNIPROT:Q05017; GB:Z12841; NID:g1689; PIDN:CAA78303.1; PID:g1690 C;Keywords: hydrolase</bol>
Que Bes Mat	Query Match Best Local Sin Matches 368;	Query Match Best Local Similarity 73.3%; Pred. No. 4e-145; Matches 368; Conservative 39; Mismatches 62; Indels 33; Gaps 2;
දි දි	1 1	MRELVGSGRYDTGEDFSVVLQPFFQNIQLPVL
\$ g	33	Alepigsktetldlraempitcptqnepplrtprnsnytypikpaienwgsdflct 88
& 8	1075 /	EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDGN 148
රු සි	149 1	LETHTTLENILKKRNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAGAWDLVERWKNSPD 208
රු සි	209	INLEKOWKLVTLFIGWDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVWVVVW 268 -
& 됨	269 1	ELASLYQGQGKCA-MLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQ 327 -
දු පු	328 1	REDFAVVVQPFFQNTL.TPLNERGDTDL.TFFSEDCFHFSDRGHAEMAIALWNNMLEPVGRK 387
È	388	TTSNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLYWAVPVAAGVGLVVGII 447

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Gaps

192 81

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A;Gene: CESP:F13H8.5
A;Introne: 46/1; 124/1; 201/3; 255/2; 419/1; 452/1; 645/3; 666/3; 692/3; 719/3; 794/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 DFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 PAQAWDLYERMKNSPDINLEKDWKLYTLFIGVNDLCHYCENP----EAHLATEYVQHIQ 247
                                                                                                                                                                                                                                                                                                                                                                                                                   276 GOGGK--CAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQREDFAV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U23139; NID:9722370; PID:9722375; PIDN:AAC46681.1; A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F13H8.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16060
R;Ding, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 GGDGNLETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 KNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 VVQPFFQNTL-TPLNERGDTDLTFFSEDCFHFSDRGHAEMALALMNNMLEPVGRKTTSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---RAFVNVVEVMELASLYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 IDKKKYFCEGLHT-FECDC--ESNKQFTDDDIQGVCFGYMMAEKDIQNTGLFDNKDDFTF
                                                                                                                                                                                                 80 NWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTA---VGARPNNSSDLPTSWR
                                                                                                                                                                                                                            24 NWSCD--ASVMAKSKKVPTSAHSVRFADIKVIGALGDSLTAANGAGAQPGDPLAVILQYR
                                                                                                                                                                                                                                                                                               138 GLSWSIGGDGNLETHTTLPNILKKFNPYLLGF----STSTWEGTAGLNVAAEGARARDM
                                                                                                                                                                                                                                                                                                                        12;
     A;Gene: CESP:W02B12.1
A;Map postition: 2
A;Introns: 5/1; 61/3; 101/1; 156/3; 212/2; 273/2; 297/3; 332/3; 368/3
A;Introns: 5/1; 61/3; 101/1; elegans hypothetical protein R07B7.8
C;Superfamily: Caenorhabditis elegans hypothetical protein R07B7.8
                                                                                                                                                     53;
                                                                                                          Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.4%; Score 414; DB 2; Length 98:
ilarity 29.8%; Pred. No. 1.7e-24;
Conservative 63; Mismatches 175; Indels
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid F13H8.
A;Reference number: Z18455
A;Accession: T16060
                                                                                                        ; Score 551.5; DB 2;
; Pred. No. 5.5e-36;
56; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-981 <DIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 FTHSRAKLKCPSPESPYLYTLRNS 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401
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                                                                                                                  21.9%;
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Query Match
Best Local Similarity 34.4%
Matches 132; Conservative
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Best Local Similarity
Matches 106; Conserv
CESP: W02B12.1
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                                                                                                                                                                                                                                                                                                                                                           82
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                                                                                                                                                                                                                hypothetical protein F09C8.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T20655
R; McMurray, A.
submitted to the EMBL Data Library, November 1995
A; Reference number: 219306
A; Accession: T20655
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-382 *WIL>
A; Residues: 1-382 *WIL>
A; Residues: 1-382 *WIL>
A; Cross-references: UNIPROT:001300; EMBL: Z68132; PIDN: CAA92221.1; GSPDB:GN00028; CESP:FC
C; Genetics:
C; Genetics:
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A;Coss-references: UNIPROT: Q23119; EMBL: Z66521; PIDN: CAA91393.1; GSPDB: GN00020; CESP: Wd A;Experimental source: clone W02B12 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPRAFVNVVEVMELASLYQGQGGK--CAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQH 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 IGGDGNLETHTILPNILKKFNPYLLGFST----STWEGTAGLNVAAEGARARDMPAQAW 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1375 TISNNFTYSRTKLKCPSPDSPYLYTLRNSRLLPDQAEADPTVLYWAVPVAAGAGLLIGIL 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein W02B12.1 - Caenorhabditis elegans Cipacies: Caenorhabditis elegans Cipacies: Caenorhabditis elegans Cipacies: Caenorhabditis elegans Cipace: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 Cipace: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 Cipacession: 726083 #shacousion 7.0 Ansecousion 7.0 Ansecousion: 726083 Anseconsion: 726083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 KASNSVPTSVHQLRPADIKVVAALGDSLT-----TAVGARPNNSSDLPTSWRGLSWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
23.8%; Score 599.5; DB 2; Length :
Best Local Similarity 37.5%; Pred. No. 7.4e-40;
Matches 132; Conservative 63; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; translated from GB/EMBL/DDBJ:Molecule type: DNA.
                                                                                             448 GTVVWRCRRGGRREDPPMSLRT
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CESP: F13H8.

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A;Cross-references: UNIPROT:Q21798; EMBL:Z75955; PIDN:CAB00117.1; GSPDB:GN00023; CESP:R0 C;Genetics:
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A;Cross-references: UNIPROT:P90862; EMBL:Z81077; PIDN:CAB03072.1; GSPDB:GN00019; CESP:F3
A;Experimental source: clone F36A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 SPDINLEKDWKLVTLFIGVND---LCHYCENPEAHLATEYVQHIQQALDILSEELPRAFV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 NVVEVMELASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEK--QELKKVNWNLQHGISSFS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 YWHQYTQREDFAVVVQPF-FQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNN 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GKFDDRE-FTVVVQPFGTEYTDAFRNEFGNYSSALYAYDVFHLGKLGQAIVAKHYWQN 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIKPAIENWGSD---FLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F36A2.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21835
                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 PDDVNSVKPHHIRVIGAMGDSLTIGYCASHFIERINGPNPGNS----FFTGIDEEI--D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNLETHTTLPNILKKFNPYLLGFSTSTWEG-TAGLNVAAEGARARDMPAQAWDLVERMKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 NKEINIEKDWKLVSLWIGTNDVGNLVFGSENPIP--VKEYKAPIEEGLLYLKKNLPRTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 PTSVHQLRPADIKVVAALGDSLTTAV------GARPNNSSDLPTSWRGLSWSIGGD
                                                                                                                                                                                                                                                     A;Map position: 5
A;Introns: 4/1; 55/3; 92/1; 148/3; 224/2; 278/3; 336/3
C;Superfamily: Caenorhabditis elegans hypothetical protein R07B7.8
                                                                                                                                                                                                                                                                                                                                          tch 13.4%; Score 336.5; DB 2; Length 349; al Similarity 31.3%; Pred. No. 5.4e-19; 108; Conservative 51; Mismatches 133; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 MLEPVGRKTTSNNFTHSRAKLKCPSPE-----SPYLYTLRNSR 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.1%; Score 329; DB 2; L 28.0%; Pred. No. 2.9e-18; tive 62; Mismatches 137;
                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Introns: 90/2; 125/2; 196/1; 267/3; 316/2; 354/3
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               A;Reference number: Z19830
A;Accession: T24015
A;Status:
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submitted to the EMBL Data
A,Reference number: Z19476
A,Accession: T21835
                                                                                                                                               A; Residues: 1-349 <WIL>
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C; Accession: T24015
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Best Local
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: TS-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
C;Accession: T24016
R;Harris, B.
submitted to the EMBL Data Library, July 1996
A;Reference number: 219830
A;Reference number: 219830
A;Accession: T24016
A;Residues: 1-348 <WIL>
A;Molecule type: DNA
A;Residues: 1-348 <WIL>
A;Residues: 1-348 <WIL>
A;Colectics: Cione R07B7
C;Genetics: C;Genetics: Clone R07B7
C;Genetics: CRSP:R07B7
A;Gene: CRSP:R07B7
A;Map position: 5
A;Introns: 4/1; 55/3; 91/1; 147/3; 223/2; 277/3; 335/3
C;Superfamily: Caenorhabditis elegans hypothetical protein R07B7.8
                                          321
                                                                                                      381
                                                                                                                                          -OKYGNSSTFAVVIAPAMDLKSIPL-LKNOPNIGLLALDCFHLSPIAHDIAAKOIWKGLF 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 IKPAIENWGSDFLCTEWKASNSV-----PTSVHQLRPADIKVVAALGDSLTTAVGARPN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 NSSDLPTSWRGLSWSIGGDGNLETHTTLPNILK----KFNPYLLGFSTSTWEG-TAGLNV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAEGARARDMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVND---LCHYCENPEAHLA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 DEYKSHIEKGLLYLKENLPRIVSIVGMFPAOLLOEAO-----SILKNGKRA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 LEKQELKKVNWNLQHGISSFSYWHQYTQR---EDFAVVVQPF-FQNTLTPLNERGDTDLT 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 NIVGQRQRYPGNAFFTGMDFEVDRHLTVYNIFRIJAEKTGNKLFGGSTGIDYGENTGLNV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 TEYVQHIQQALDILSEELPRAFVNVVEVMELASLYQGQGGKCAMLAAQNNCTCLRHSQSS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T24015
hypothetical protein R07B7.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: La-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                 VVEVMELASLYOGOG-GKCAMLAAQNNCTCLRHSQSSLEKQELKK-VNWNLQHGISSFSY
                                                                                                    WHOYTOREDFAVVVOPFFONTLIPLNERGDIDLIFFSEDCFHFSDRGHAEMAIALWNNML
                                                                                                                                                                                                               EPVGRKTTSNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEEAPEVLYWAVPVA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 16.1%; Score 406.5; DB 2; Local Similarity 32.2%; Pred. No. 1.5e-24; Nes 117; Conservative 66; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRL 418
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Gaps

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Indels

Length 425;

187 Qy 360DCFHFSDRGHAEMAIALWINMLEPVGRKTTSNNFTHSRAKIKC 402 228 DD 1021 KLAVNVIVHDIFYAFDVIQGNHSKFTTNLQKEVIISPHYFAHCLSEVVC 1069	PRESULT 9 S75251 hypothetical protein slr1028 - Synechocystis sp. (strain PCC 6803) C,Species: Synechocystis sp. A,Variety: PCC 6803 C,Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 C,Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 C,Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 S,Roton S75251 R,Raneko, T.; Bato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N. K, Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud MR, Res. 3, 109-136, 1996 A,Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti	вћ, S.V. 6; SPDB:	22; RESULT 10 3C7672 catalase (EC 1.11.1.6) - Des Catalase (EC 1.11.6) - Des Catal	
130 SDLPTSWRGLSWSIGGDGNLETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGA - - - - - - - - - - - - -	RARDMPAQAWDLVERMKKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVOHIO	Oy 359 EDCFHESDRGHAEMAIALWNNMLEPVGRKTTSNNFTHSRAKLKCPS 404 S19 EDCFHESDRGHAEMAIALWNNMLLEPVGRKTTSNNFTHSRAKLKCPS 422 BD 379 RDKPLINRRGHNYATKWLWNRLIG-GDLYNLSSATLSQDNYFCPS 422 RESULT 8 TRAP-like protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Gateries to the EMBL Data Library, November 1995 A;Genteile Data Library, November 1995 A;Accession: T38084 A;Accession: T380	Query Match 4.2%; Score 107; DB 2; Length 3655; Best Local So.4%; Pred. No. 31; Best Local Sometive 63; Mismatches 169; Indels 146; Gaps Matches 97; Conservative 63; Mismatches 169; Indels 146; Gaps 24 FONIQLPVLALEPLGSKTETLDLRAEMPITCPTONEPFLR 54 FONIGLREPLISRIEELGSSDIRHGSVLLRIERLSFVTVSMFATENEPVLREFVSEI 645 FLNILLRPPLLSRIEELGSSDIRHGSVLLRIERLSFVTVSMFATENEPVLREVVSEI 64TPRNSNYTYPIRPAIENWGSDFLCTEWKASNSVPTSVQLRADIRVVAA 701 IVKCMKLAPNSANSINYYYLLRALFRGIGGGRFESLYKEVMPLLHALLEAFNSLL D 701 IVKCMKLAPNSANSINYYYLLRALFRGIGGGRFESLYKEVMPLLHALLEAFNSLL	114 IGDSLTTAVGARPNNSSDLPTS

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endopoptidase [imported] - Staphylococcus aureus (strain N315)
Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
CiAccession: F89819
R;Kuroda, M; Ohta, T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L; Oguc
R;Kuroda, M; Ohta, T; Kobayashi, N; Sawano, T; Inoue, R; Kaito, C; Sekimizu, K;
C; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Fitle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-818 «KUR>
A;Residues: U-818 «KUR>
A;Experimental source: uniPROT:Q99W78; GB:BA000018; PID:g13700415; PIDN:BAB41713.1; GSPDB:G
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 GELOCIGATTLDEYRKNIEKDAALERRFQPVQVDEPSVVDTVAILKGLRD-----RYEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 PNILK---KFNPYLLGFSTSTWEGTAGLNVAAEG-ARA------RDMPAQAWDL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.9%; Score 99; DB 2; Le 21.6%; Pred. No. 15; ive 51; Mismatches 119;
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A;Molecule type: DNA
A;Residues: 1-913 <GEI>
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C;Superfamily: endopeptidase Clp ATP-binding chain
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DAVNSISKAVRRARAGLKDPKRPIGSFIF
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: C87618
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87618
A;Accession: C87618
A;Residues preliminary
A;Residues: 1-749 <ATOA
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C;Genetics:
A;Gene: CC2981
C;Superfamily: excinuclease ARC chain R
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                                                                                  201 FISPDNQRYWVKFHLRTQQGIKNLTDAEAEAIVARDRESHQRDLYDSIERGDFPRWTNYV 260
                                                                                                                                                         : ||| ::|| |: || | 261 QVMPEKDAEKLPYHPFDLTKVWFHKDCPLIEVGVLEL---NRNPE----NYFAEVEQA- 311
                                                                                                                                                                                                                                                                     362
    --RGIPASYRHMH----GFGS----HTFS 200
                                                                                                                                                                                                                                                                                                         296 SOSSLEKQELKKVNWNLQHGISSFSY----WHQYTQREDFAVVVQPFFQNTLTPLNERGD 351
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                                                                                                                                DINLEKD--------KLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQAL
                                                                                                                                                                                                                     DILSEELPRAF--VNVVEVMELASLYQGQG-------GKCAMLAAQNNCTCLRH
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                                           NILKKFNPYLLGFSTSTWEGTAGLNVA-AEGARARDMPAQAWDLVE-
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  ----VTVVMSD----
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  PEALHQ---
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LPVLALEPLGSK-TETLDLRAEMPITCPTONEPFLRTPRNSNYTYPIKPAIENWGSDFLC
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                                                            TEWKASNSVPTSVHQLR-
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1804 <STR>
A;Cross-references: UNIPROT.Q9Z1Q1; EMBL:AF110498; MID:g4063502; PID:g4063503; PIDN:AACS
A;Experimental source: cell line BHK-21
A;Cross-references: UNIPROT:001922; EMBL:AF003390; NID:g208866; FID:g208867; PIDN:AAB$
A;Experimental source: strain Bristol N2; clone R155
C;Genetics:
A;Gene: CESP:R155.4
A;Map position: 3
A;Introns: 47/1; 68/1; 335/1; 719/1; 794/2; 864/1
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R.Steinert, P.M.; The Library, December 1998
Bubmitted to the EMBL Data Library, December 1998
A,Description: A high molecular weight intermediate filament associated protein in BHK. A,Reference number: 221538
A,ACCESSION: T34518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                --- OPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAI-- 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ALWNNMLEPVGRKTTSNNFTHSRAKLKCPSPESPYL-YTLRN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 SVLKLMEAANSNSLAGLLPILNN-LESIGLNFSSSSFSKSKQSLKVLDTSFASLNNTINN 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 ELASLYÇÇÇĞĞKCAMLAAQNNCTCLRHŞQSSLEKQELKKVNWNLQHGISSFSYWHQYTQR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         658 KNMKVLIGLGDELEKLLSDLNLFVKSVKPSNSTNLADFAGIFBAARVKGVPHNFMAIKA 717
                                                                                                                                                                                                                                                                                                                                               INLEXDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVM 268
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                                                                                                                                                                                                                                            SVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDGNLETHTTLPNI 158
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                                                                                                                                                                                                                                                                                              LKKFNPYLLGFSTSTWEGTAGLNVAAE------GARARDMPAQAWDLVERMKNSPD
                                                                                                                                             RELVGSGRYDTO-EDFSVVLQPFFQNIQ-----LP------VLALEPLGSKT
                                                                                                                                                                                                                      435 VALN---EM----VKTIND---LKKKDNSDALQRMSTIVDGVNNTNYDGKLQEYKASKDFPV
                                                                                                                     Gaps
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22.0%; Pred. No. 48;
cive 53; Mismatches 156; Indels 134;
                                                                                                                       Indels 160;
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48;
                                                                                             Length 913;
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3.9%; Score 99; DB 2; Le
Best Local Similarity 21.1%; Pred. No. 17;
Matches 116; Conservative 72; Mismatches 202;
                                                                                             DB 2;
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Dest Local Similarity 22.0%
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cf-9 protein precursor - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 20-Jan-1995 #sequence_revision 20-Jan-1995 #text_change 15-Mar-2004
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                                                                                                                                                                       136 WRGLSWSIGGDGNLETHTTLPNILKKFNPYLLGFSTSTWBGTAGLNVAAEGARA-RDMPA
                                                                                                                                                                                                                                                                                                                                          195 QAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQ-----QA
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----PADIKVVAALGDSLTT----AVGARPNNSSDLPTS
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3.9%; Score 98.5; DB 2; Length 863;
Best Local Similarity 19.9%; Pred. No. 18;
Matches 98; Conservative 59; Mismatches 167; Indels 169;
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233 ERVFHLSNLQSLHLSVNPQLTVRFPTTKMNSSASLMTLYVDSVNIADRIPKSF 285	LAAQNNCTCLRHSQSSLEK	286SHLTSLHELYMGRCNLSGPIPKPLWNLTNIVFLHLGDNHLEGPISHFTIFEKLKRL 341	308 VNWNLQHGISSFSYWHQYTQREDFAVVVQPFFQNTLTPLNERGDTDLTFFSEDCF 362	342 SLVNNNFDGGLEFLSF-NTQLERLDLSSNSLTGPIPSNISGLQNLECL 388	363 HFSDRGHAEMAIALMNNMLEPVGRKTISNNFTHSRAKLKCPSPE 406	389 YLSS-NHINGSIPSWIFSLVELDLSNYTFSGKIQEFKSKTLSAVTLKQNKLKGRIPN 447	407 SPYLYTLRNSRIL 419	448 SILNQKNLQLL 458	
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     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Q9N4P5
Q965W0
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ALIGNMENTS

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MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg N.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Scapleton M., Soares M.B., Donahold M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

Miting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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Genew, HGNC:30041; PLB1.
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPRO01087; Lipase GDSL.
Pfam; PF00657; Lipase GDSL; 1.
SEQUENCE 423 AA; 47354 MW; A20A193491BA780C CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
       423 AA
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Best Local Similarity 99.8<sup>3</sup>
Matches 422, Conservative
PRELIMINARY;
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50 MPITCPTQNEPFLRIPRNSNYTYPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIK 109

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REDFAUVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMALALWNNMLEPVGRK 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 LETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPD
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butherla; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                        Cytoplasmic (Potential).
4 X 308-326 AA approximate repeats.
                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1458;
                                                                                                                                                                                                                                                                                                                                                9D1608F47B1062E6 CRC64;
                                                                                                                Phospholipase ADRAB-B.
Extracellular (Potential)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                                                                                                       ; Score 1933.5; DB 1 ; Pred. No. 1.7e-141; 39; Mismatches 62;
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                                                                                                                                                                                                                                                                                          similarity.
similarity.
similarity.
                                                                                    Repeat; Signal; Transmembrane.
                                                                                                                                                               Potential
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                                                                                                      Potential
InterPro; IPR001087; Lipase GDSL.
InterPro; IPR008265; Lipase_GDSL_AS.
Pfam; PF00657; Lipase GBSL, 3.
PROSITE; PS01098; LIPASE GDSL SER; 2.
Hydrolase; Repeat; Signal; Transmembr.
SIGNAL
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(TrEMBLrel.
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Phospholipase B.
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**MEDLINE=93286138; PubMed=8509424;

**MEDLINE=93286138; PubMed=8509424;

**Boll W.**, Schmid-Chanda T.**, Semenza G., Mantei N.;

**MEDLINE=93286138; PubMed=800 in intestine of adult but not baby rabbits.

**Teolarion of cognate cDNAs and characterization of a novel brush to reduction of cognate cDNAs and characterization of a novel brush to respect to the selectase and phospholipase activity.";

**Jerior Chem.** 268:12901-12911(1993).

**Jerior Chem.** 268:12901-12911(1993).

**Jerior Chem.** 268:12901-12911(1993).

**Jerior Chem.** 268:12901-12911(1993).

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**Jerior Chem.** 268:12911(1993).

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01-FEB-1994 (Rel. 28, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Phospholipase ADRAB-B precursor (EC 3.1.-.-).
Oryctolagus metalculus (Rabbit).
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SIMILARITY: Belongs to the "GDSL" lipolytic enzyme family.
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EMBL; Z12841; CAA78303.1; -.

PIR; A45665; A45665

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Name=LOC388937;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 66.9%
Matches 327; Conservative
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XX MEDLINE=98256256; PubMed=9593672; DOI=10.1074/jbc.273.22.13407;
XA Delagebeaudeuf C., Gassama-Diagne A., Nauze M., Ragab A., Li R.Y.,
AD Elagebeaudeuf C., Gassama-Diagne A., Nauze M., Ragab A., Li R.Y.,
XA Capdevielle J., Ferrara B., Fauvel J., Chap H.;

R. Capdevielle J., Ferrara P., Fauvel J., Chap H.;

R. Possible role in sperm maturation and activation by limited
XT B. Possible role in sperm maturation and activation by limited
XT D. Possible role in sperm maturation and activation by limited
XL J. Biol. Chem. 273:13407-13414(1998).

R. D. Biol. Chem. 273:13407-13414(1998).

R. D. Biol. Chem. 273:13407-13414(1998).

R. D. Biol. Chem. 273:13407-13414(1998).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MELASLYQGQGGXC-AMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QREDFAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNMLEPVGR 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1014 LWVNMLEPVGSKTDTLDLTADISLPCPTQEEPFLRTPQNSDYTYPTKPAIENWGSDFLCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ALEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipase B.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chondata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                     70.1%; Score 1764; DB 2; Length 1463; 68.9%; Pred. No. 2.8e-128; ive 41; Mismatches 78; Indels 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRELVGSGRYDTQEDFSVVLQPFFQNIQLPVL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 VVGIIGTVVWRCRRGGRREDPPMSL 467
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 68.9
Matches 348; Conservative
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01-JUN-1998 (TrEMBLrel.
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                                     SEQUENCE
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1D O554728

1D O55050

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MEDLINE-98113187; PubMed-9942065; DOI=10.1074/jbc.273.4.2222;

Takemori H., Zolotaryov F.N., Ting L., Urbain T., Komatsubara T.,

A Hatano T., Okamoto M., Tojo H.;

"Identification of functional domains of rat intestinal phospholipase in a flequification of functional domains of rat intestinal phospholipase B/lipase. Its cDNA cloning, expression, and tissue distribution.";

B/lipase. Its cDNA cloning, expression, and tissue distribution.";

B/lipase. Its cDNA cloning, expression, and tissue distribution.";

B/lipase. Its cDNA cloning, expression, and tissue distribution.";

R GO; GO:0003824; Focatalyty; IEA.

R InterPro; IPR001087; Lipase GDSL.

R InterPro; IPR001087; Lipase GDSL.

R PROSITE; PS01098; LIPASE GDSL.3.

R PROSITE; PS01098; LIPASE GDSL.3.

R PROSITE; PS01098; LIPASE GDSL.3.

R PROSITE; PS01098; LIPASE GDSL.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LETHTTLPNILKKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELASLYQGQGGKCAM-LAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYWHQYTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REDPAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNNMLEPVGRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ALEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 1450;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.1%; Score 1715.5; DB 2;
66.9%; Pred. No. 1.7e-124;
ative 53; Mismatches 76;
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Created)

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RESULT 7
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                                   WELLIE-STABBEST; PubMed=12477932; DOI=10.1073/pnas.242603899;

MELLINE-STABBEST; PubMed=12477932; DOI=10.1073/pnas.242603899;

A trausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Millahy S.J.,
A Raha S.S., Mordellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
A Richards S., Worlby K.C., Hale S., Garcia, Garcia, C., Gubs R.A.,
A Villalon D.K., Murny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
A Nillalon D.K., Murny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
A Nillalon D.K., Murny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
A Nillalon B.K., Marny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
A Nillalon B.K., Murny D.W., Sodergren E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Kreywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 WKASNSVPISVHQLRPADIKVVAALGDSLI--TAVGARPNNSSDLPTSWRGLSWSIGGDG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLETHTILPNILKKENPYLLGFSTSTWEGT---AGLNVAAEGARARDMPAQAWDLVERMK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 LEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNY-TYPIKPAIE---NWGSDFLCTE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VTVLEIVNLRELYQEKKVYCPRMILRSLCPCVLKFDDNSTELATLIEFNKKFQEKTHQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 YWHQYTQREDFAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMAIALWNNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEPVGRKTTSNNFTHSRAKLKCPSPESPYLYTLRNS-----RLLPDQAEEAPEVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.4%; Score 841; DB 2; Length 48
44.5%; Pred. No. 6.1e-57;
ive 64; Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR001087; Lipase_GDSL.
InterPro: IPR001087; Lipase_GDSL_AS.
Pfam. PR00657; Lipase_GDSL.1.
PROSITE; PS01098; LIPASE_GDSL_SER; 2.
SEQUENCE 488 AA, 5434I MW; GBE12FF5CB0AC9C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC065041; AAH65041.1; -. GO; GO:0003824; F:catalytic activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.4
Query Match
Best Local Similarity 44.5
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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STRAIN=FUBN-3: TISSUE=Mammary tumor;

STRAIN=FUBN-3: TISSUE=Mammary tumor;

STRAIN=FUBN-3: PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.A.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B. Scheetz T.E.,

B. Stonstein M.J., Ugdin T.B., Toshiyuki S., Garninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,

R. Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Willalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

R. Willalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

R. Willadon B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Krzwinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Rodriguez A.C., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 QELKKVNWNLQHGISSFSYWHQYTQREDFAVVVQPFFQNTLIPLNERGDTDLIFFSEDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 HFSDRGHAEMAIALWNNMLEPVGRKTTSNNFTHSRAKLKCPSPESPYLYTLRNSRLLPDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 YFSDRGHAEMAIALWINMLEPVGWKTSSINFIYNRTKLKCPSPERPFLYTLRNSCLLPDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 QELKKLINWNLQSGISELSYWHRYMEREDFAVTVQPFFRNTFIPLNEREGLDLTFFSEDCF
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TAXID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=FVB/N-3; TISSUE=Mammary tumor;
STRAIN=FVB/N-3; TISSUE=Mammary tumor;
Director MGC Project;
Submitred (JUL-2015) to the EMBL/GenBank/DDBJ databases.
EMBL, BC033606; AAH33506.1;
MGD; MGI:2387632; BC033606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 AA; 21471 MW; 56153A6266A22315 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein F09C8.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                  FROM N.A.
UR/N-3; TISSUE=Mammary tumor;
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01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
BC033606 protein.
                                                                                                                                                Mus musculus (Mouse)
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Matches 116;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 SPD-INLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSEELPRAFVNV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 VEVMELASLYQGQGGK--CAMLAAQNNCTCLRHSQSSLEKQELKKVNWNLQHGISSFSYW 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 HQYT-----QREDFAVVVQPPFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMA 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 KASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDGNLE
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 374;
                                                                                                                             "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 TYLWINILQPVGSKSTVSNMSVPLQTLACPDAACPFIRTPKNSQ 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 AA; 41921 MW; 553E0DB7EE3A41EC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                                                                          McMurray A.A.; Submitted (NOV-1995) to the EMBL/GenBank/DDB EMBL, Z66132; CAA92221.2; PIR; T20655; T20655. WormBase; WBGene00008621; F09C8.1. WormPep; F09C8.1; CE31470. GG.0003824; F:catalytic activity; IEA. InterPro; IPR001087; Lipase GBSL. Pfam; PF00657; Lipase GBSL;
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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MEDLINE=99069613; PubMed=9851916;
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Science 282:2012-2018(1998).
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Matches 132; Conservative
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Caenorhabditis elegans.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 PAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENP-----EAHLATEYVQHIQ 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 AAVQILQDNLPRTIVSLTGMFNMRMLRKIDKKKYFCEGLHT-FECDC--ESNKQFTDDDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 NWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTA--VGARPNNSSDLPTSWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 NWSCD--ASVWAKŠKKVPTSAHSVRFADIKVIGALGDSLTAANGAGAQPGDPLAVILQYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 QALDILSEELPRAFVNVVEVMELASLYQGOGGK--CAMLAAQNNCTCLRHSOSSLEKQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 KKVNWNLQHGISSFSYWHQYTQREDFAVVVQPFFQNTL-TPLNERGDTDLTFFSEDCFHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgCP5492 (Fragment).
Name-agCG5300; ORFNames=ENSANGG0000018581;
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAYGHGNIGMHLMNTIVQPVGFKQTSVNLSDPSVGLHCPSTNCPFFPTTKNS 369
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.9%; Score 577.5; DB 2; Length 382; Best Local Similarity 37.5%; Pred. No. 1.5e-36; Matches 132; Conservative 56; Mismatches 143; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDRGHAEMAIALWINMLEPVGRKTTSINNFTHSRAKLKCPSPESPYLYTLRNS
                          Swinburne J., Ainscough R.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                           11 protein.
382 AA; 41772 MW; 6430145B8E525CA3 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                               Wormbery, WOSD12.1, CR03761.
GO, GO:0003824; F:catalytic activity; IEA.
InterPro; IPR001087; Lipase GDSL.
Hypothetical protein.
SEQUENCE 382 AA; 41772 MW; 6430145B8BS
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Pfam; PF00657; Lipase GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
NON TER.
SEQÜENCE 348 AA; 39561 MW; F77477
                                                                          EMBL; Z66521; CAA91393.2; -.
PIR; T26083; T26083.
WormBase; WGGene00012201; W02B12.1.
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STRAIN=Bristol N2;
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                                                                                                                                                       Q7PCU2
                                                                                                                                    RESULT 11
Q7PCU2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTLPNILKKFNPYLLGFSTS---TWEGTAGLNVAAEGARARDMPAQAWDLVERMKNSPDI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLEKDWKLVTLFIGVNDLCHY---CENPEAHLATEYVQHIQQALDILSEELPRAFVNVVE 266
                                                                                                                                                                       QHGISSFSYWHQYTQREDFAVVVQPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEM 372
                  11;
                                                                           200
                                                                                                 131
                                                                                                                  ERMKNSPDINLEKDWKLVTLFIGVNDLCH---YCENPEAHLATEYVQHIQQALDILSEEL 257
                                                                                                                                 PRAFYNVV--EVMELASLYQGQGGKCAMLAAQNNCTCLRHSQSSLEKQELKKV--NWN-L 312
                                                                                                                                                                                                               143
                                                       71
                                                                           GGDGNLETHTTLPNILKKFNPYLLGFSTSTWEGT--AGL-NVAAEGARARDMPAQAWDLV
                                                                                        Gaps
                                                   12 FFCNTTGMRSETVPTSVDRLRPGDIDIIGAIGDSLTAGNGAMATNILEVLIENKGLSWSI
                                    FLC-TEWKASNSVPTSVHOLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSI
                                                                                                                                                                                                                                                                                                                                                                               Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles Genome Sequencing Consortium;
Anopheles Genome Sequencing to the BMBI/Genbank/DDBJ databases.
Submitted (APR-2003) to the BMBI/Genbank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which
 Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.4%; Score 563; DB 2; Length 331; 39.4%; Pred. No. 1.7e-35; rive 54; Mismatches 133; Indels
                                                                                                                                                                                                                                                     AIALWINMLEPVGRKTTSNNFTHSRAKLKCPSPESPYLYTLRNS 416
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 AA; 37931 MW; 9B872EBF521D706D CRC64;
                                                                                                                                                                                                                                                                                                                                            01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) ENSANGP00000025054 (Fragment).
22.9%; Score 575.5; DB 2;
39.8%; Pred. No. 2e-36;
iive 56; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AAABB1008956; EAA44293.1; -. GOOSSE, F:catalytic activity; IEA. GO; GO:0003824; F:catalytic activity; IEA. InterPro; IPR001087; Lipase_GDSL. Pfam; PF00657; Lipase_GDSL;
                                                                                                                                                                                                                                                                                                                 331
                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132; Conservative
             Best Local Similarity 39.8
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Matches
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Q7PI39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 LEKDWKLVTLFIGVNDLCH---YCENPEAHLATBYVQHIQQ-----ALDILSBELFRAFV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104
                                                                                                                         240 SREFRGLDEFAVVYQPWSLAVTWKMNGK-DIDYSLLSYDCFHMSQKGNAFAGTALWNNML 298
VMELAS--LYQCQGGKCAMLAAQNNCTC---LRHSQSSLEKQELKKVNWNLQHGISSFSY 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 LEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCTEWKAS
                                       181 VPSVAKVVMLQRKPFACESL-HHGECSCWIGKLYNQSEASRDRWARIQDEYIRVEKEVÄE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                              WHQYTQREDFAVVVOPFFQNTLTPLNERGDTDLTFFSEDCFHFSDRGHAEMALALWINML
                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
04-WAR-2004 (TrEMBLrel. 26, Last annotation update)
04-MAR-2004 (AGCP033).
Name-agCG44667; Synonyms=agCG45512; ORFNames=ENSANGG0000012533;
Anopheles gambiae str. PEST.
Rukaryota; Meta2coa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles Genome Sequencing Consortium, Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.2%; Score 560; DB 2; Length 37 36.8%; Pred. No. 3.5e-35; ive 46; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AARDOLO06916; EAA09798.1; -. GO, GO:0003824; F:catalytic activity; IEA. InterPro; IPRO01087; Lipsse GDSL. InterPro; Lipsse GDSL. SEQUENCE 373 AA; 42957 MW; C31C5B6C99A164B1 CRC64;
                                                                                                                                                                                            EPVGRKTTSNNFTHSRAKLKCPSPESPYLYTLRNS 416
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Matches 149; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data
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182 VAAEGARARDMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPE--AHLA 239
                              153 QAVPGAQAADIIIQARALVQIMQNHRDIDIKNDWKLINVFIGANDMCRYCEEKENGIHSK 212
                                                                                            240 TEYVQHIQQALDIISEELPRAFVNVVEVMELASLYQGQGGK--CAMLAAQNNCTCLRHSQ 297
                                                                                                                        SSLEKQELKK----VNWNLOHGISSFSYWHQYTQREDFAVVVQPFFQN-TLTPLNERGDTD 353
                                                                                                                                                                                                                                270 SSFTNDDVSQACHLYMDAQOEIQDSGI----FDTSDDFTFVLQPFFNGITIPPLKPDGEVN 326
                                                                                                                                                                                                                                                                                                       | :|: ||||| ||| ||| :| |||| ||| || 327 LDWFAPDCFHFSRLGHANVARHLWNIVQPVGSKNHIVNLSDPTIPLNCPDATCPFIRTT 386
                                                                                                                                                                                                                                                                                LTFFSEDCFHFSDRGHAEMAIALWNNMLEPVGRKTTSNNFTHSRAKLKCPSPESPYLYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
14 potchetical protein Y6584BR.1.
Name=Y6584BR.1; ORFNames=Y6584BR.1;
Caenorabablitis elegans.
Elkaryota, Metazoa; Nemacoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Maupin R., Bauer C.;
"The sequence of C. €
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STRAIN=Bristol N2;
Waterston R.H.;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                  KNS 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 SLDEHVTVASENFTLNLEQTSAFAIMQLLADVMKKFSPNIMGYSTGIGSANVWE-VSKLN 152
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                                                                                                                                                                                                                         Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                      mosimization equipolitium, in the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 398;
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al Similarity 35.5%; Score 559.5; DB 2; Length 3
al Similarity 35.5%; Pred. No. 4.1e-35;
129; Conservative 61; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of C. elegans cosmid Y73B6BL.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, ACO84197; AAM4393.1; --
Wormbase; WEGene00022256; Y73B6BL.37.
Wormpep; Y73B6BL.37; CE29331.
GO; GO:0003874; F: Catalytic activity; IEA.
InterPro; IRR01087; Lipsee GDSL.
Pfam; PP00657; Lipsee GDSL, 1.
Hypothetical protein:
SEQUENCE 398 AA; 44003 MW; E6027C51E47E2B76 CRC64;
                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Y73B68L.37.
Name-Y73B6BL.37; ORFNames=Y73B6BL.37;
                                               398 AA
                                               PRT;
                                                                                                                                                                                                                                                                                                                                         STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                            PRELIMINARY;
                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.;
Submitted (MAY-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson R.;
Submitted (JUL-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R.;
Submitted (JUN-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Bristol N2;
WormBase Consortium;
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RESULT 12
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21.7%;
37.5%;
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                                                                                                                                                                                                                                                                                                          Best Local Similarity 37.5
Matches 126; Conservative
                PRELIMINARY;
                                     01-MAR-2004 (TrEMBLr:
01-MAR-2004 (TrEMBLr:
01-MAR-2004 (TrEMBLr:
EDiplo16 (Fragment).
Name=ebiG1016; ORFNa
                                                                                                                                          SEQUENCE FROM N.A.
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ID 0707K2
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 VQHIQQALDIILSEELPRAFVNVVEVMELASLYQGQGGK--CAMLAAQNNCTCLRHSQSSL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------NTDİSAACHLYMDAQQEIQDSGIFDSTDÖFTFVVQPFFNGITVPPLKP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 YPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 LPT--SWRGLSWSIGGDGNLETHTTLPNILKKFNPYLLGFST----STWEGTAGLNVAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGARARDMPAGAMDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPE--AHLATEY 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 YP-----GWQCD--ASLYQKSKNTPTSAHSVRFTDIKVLGALGDSLTAANGAGAPKGDP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 RGDTDLTFFSEDCFHFSDRGHAEMAIALWNNMLEPVGRKTTSNNFTHSRAKLKCPSPESP
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                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
21.9%; Score 552; DB 2; Length 377
Best Local Similarity 35.9%; Pred. No. 1.5e-34;
Matches 132; Conservative 59; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases.
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                                                                                                        the EMBL/GenBank/DDBJ databases
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WORDBASE; WEGENEO0022040; Y65B4BR.1.
WORDPEP; Y65B4BR.1; CE252040; Y65B4BR.1.
InterPro; IPR001087; Lipase_GDSL.
InterPro; IPR0657; Lipase_GDSL.
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
  Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                     to the EMBL/GenBank/DDBJ databases
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FFRTTKNS 368
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STRAIN=Bristol N2;
Wilson R.;
Submitted (DEC-2003) to
                                                                                                                                                     Waterston R.;
Submitted (NOV-2002)
                                                                                                                                                                                                        Waterston R.;
Submitted (JAN-2003)
                                                  Waterston R.;
Submitted (NOV-2001)
                                                                                                                                                                                                                                                                                                           WormBase Consortium;
                                                                                                           Submitted (MAY-2002)
                                                                          SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
                                                                                                                                SEQUENCE FROM N.A.
STRAIN-Bristol N2;
                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-Bristol N2;
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                           SEQUENCE FROM N.A.
STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 DWKLVTLFIGVNDLCHY---CENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVMEL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 RGLDEFAVVHQPWTRN--LSLMKGNEVDYTLLSYDCFHNSQKGHAQAAIAYWNNLLEFPG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 NILKMFNPKLVGYSYRDSYSFHWDSQFNNAEIGAVSKELPHWAAQMVTRIRTDKRVNFQK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 ASL--YQGQGGKCAMLAAQNNCTCL---RHSQSSLEKQELKKVNWNLQHGISSFSYWHQY 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 STVVSIKKKPMMCWIL-HHAECPCWVGPLHNSTKESRARWARIQTQYRKVEBEVAMLDEF 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 PTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDGNLETHTTLP
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01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Blip652 (Fragmen)
Name=ebiG652; ORFNames=ENSANGG00000000587;
Anophales gambiae str. PEST.
Anophales gambiae str. PEST.
Neoptera; Endopterygota; Arthropoda; Hexapoda; Insecta; Prerygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anophales.
NCBI TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                  Anopheles gambiae str. PEST.

Eukaryota; gambiae str. pest.

Bukaryota; Metazoa; Atrinopoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                   Anopheles Genome Sequencing Consortium, Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 330 37624 MW; 8D6235983BE92571 CRC64;
                                                          Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 RKTTS-----NNFTHSRAKLKCPSPESPYLYTLRNS 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 545.5; DB Pred. No. 4e-34;
330 AA
                                                                                                                  ORFNames=ENSANGG0000000884;
                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.
EMBL, AARBO1008956; EAA10654.1; -.
GO, GO:003824; F:catalytic activity; IEA.
Interpro; IPR001087; Lipase_GDSL.
Pfam; PF00657; Lipase_GDSL; 1.
                                            Created)
PRT;
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SEQUENCE FROM N.A.
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97 PTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGGDGNLETHTTLP 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DWKLVTLFIGVNDLCHY---CENPEAHLATEYVQHIQQALDILSEELPRAFVNVVEVMEL 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 RGLDEFAVVHQPWTRN--LSLMKGNEVDYTLLSYDCFHMSQKGHAQAAVAYWNNLLEPPG 301
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                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 21.6%; Score 544.5; DB 2; Length 330; Best Local Similarity 37.2%; Pred. No. 4.7e-34; Matches 125; Conservative 64; Mismatches 120; Indels 27;
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STT BRACCCC REASON STATES
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Human phospholipase b-like polypeptide and uses thereof
Patent: WO 02062977-A 3 15-AUG-2002;
PE Corporation (NY) (US)
Location/Qualifiers
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Sequence 3 from Patent WO02062977.
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721 IACTGCTTAGGCAGCTCAGCCTCTCAAGAGGGAAGAGCAGCTGGTGTGATGTGGCGTTGA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. [bases 1 to 180465]
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 [11], 1097-1108 (1998)
AC074011 180465 bp DNA linear PRI 07-N
Homo sapiens BAC clone RP11-780J6 from 2, complete sequence.
AC074011
                                                                                                                                                                                                                                         2 (bases 1 to 180465)
Paulson, E., Cotton, M. and Lohmeyer, A.
The sequence of Homo sapiens BAC clone RP11-780J6
Unpublished
                                                                 AC074011.5 GI:15144519
                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 180465)
Waterston, R.H.
                                                                                    HTG.
Homo sapiens (human)
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SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscogawa, K., Woon, P. Y., Zhao, B., Frengen, B., Tateno, M., Catanes, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5::1-8. The clone may be obtained either from libraries Genetics 1:1-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer Institute

(http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VECTOR: PBACE3.6
NEIGHBORING SEQUENCE INFORMATION:
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is AC022076. Actual start of this clone is at base position 1 of RP11-780J6; actual end is at base position 1 sequence of RP11-780J6.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MCPherson, Department of Genetics, the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63108, USA
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                                                          Louis,
                                                                                                                                                                                                                                                                                  Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108,
    Submitted (09-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston,R.
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Contact: Summary Statistics
Center project name: H_NH0780J06
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332. .651
/rpc_family="Alu"
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/rpc_family="Alu"
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3140. .3189
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Submitted (09-AUG-2001)
University, 4444 Forest
5 (bases 1 to 180465)
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Waterston, R.
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RS Birren, B., Nusbaum, C., Lander, E., ADOUBLIELL, H., ALLEN, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Boguslavkiy, L., Boukhgalter, B., Carum, B., Dearfaellano, Y., Farrelano, S., Collymore, A., Cook, A., Cooke, P., Corum, B., Dardellano, J., Farco, S., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Farreira, P., FitzGerald, M., Hafez, N., Hagopian, D., Hagos, B., Grand-Dierre, N., Hafez, N., Hagopian, D., Hagos, B., Lindblad-Toh, K., Liu, G., Lui, A., Mathews, C., McCarthy, M., Madordan, P., Manous, L., Mahon, T., Mabbitt, R., Machean, C., McCarthy, M., Major, J., Manning, J., Matthews, C., McCarthy, M., Major, J., Manous, T., Mlenga, V., Murphy, T., Naylor, J., Nelus, T., Miool, R., Morbu, C., O'Connor, T., O'Donnell, P., Najor, J., Nobu, C., O'Connor, T., O'Donnell, P., Najor, J., Schauer, S., Schubback, R., Steta, R., Rise, C., Rogov, P., Rachnyka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachnyka, A., Ramasamy, U., Raymond, C., Retta, R., Travers, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Mu, A., Lepeats were identified using RepeatMasker: All repeats were identified using RepeatMasker: httml
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
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Web site: http://www-seq.wi.mit.edu
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: Project Information
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3 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Brown, A., Canarellano, K., Dewar, K., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, D., Galagan, J., Gardyna, S., Farria, P., Pitzhlay, W., Gage, D., Galagan, J., Gardyna, S., Farria, P., Fitzhlay, W., Graham, L., Grand, Pierre, N., Glide, S., Gord, S., Goyette, M., Galagan, J., Gardyna, S., Jones, C., Kamat, A., Kalas, A., Kalls, C., Lakocque, K., Jones, C., Kamat, A., Kalas, A., Kalbs, C., Lakocque, K., Jones, C., Kamat, A., Kalas, A., Kalbs, C., Lakocque, K., Jones, C., Kamat, P., McGarthy, M., McEwan, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Malthews, C., Macdonald, P., Major, J., Marquis, N., Malthews, C., McDenter, M., McDennan, P., McGarran, K., McPheeters, R., Kise, C., Rogov, P., Oliver, J., Peterson, K., Phundhang, P., Fierre, N., Pollara, V., Roman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Stauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Veller, R., Vo, A., Wilson, B., Wu, X., Waman, D., Ye, Wassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Waman, D., Ye, Wassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Waman, D., Ye, Wu, J., Young, G., Lander, Submission
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Mus musculus clone RP23-262J12, WORKING DRAFT SEQUENCE, 10
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AC102372:2 GI:30018075
HTG: HTGS PHASE1; HTGS_DRAFT.
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721 PACTOCTTCACCAGCTCACCTCACAGACCACTACACTACAGACACCTCCTCACAGACCTCACTACAGACTACACTACACTACAGACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACA
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Pred. No. 6.6e-49;
0; Mismatches 304; Indels
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contig of 1686 bp in length
gap of unknown length
contig of 1695 bp in length
gap of unknown length
contig of 2521 bp in length
gap of unknown length
gap of unknown length
contig of 3518 bp in length
contig of 3518 bp in length
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Best Local Similarity 60.1
Matches 513; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            Whe sites http://www.hgsc.bcm.tmc.edu/
Whe sites http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bom.tmc.edu
Contact: ngsc-help@bom.tmc.edu
Contert project Information
Center project name: KEHN
Center clone name: CH1310-188E12
Center clone name: CH230-188E12
Center clone name: CH230-188E12
Center clone name: Harsities
Sequencing vector: plasmid;
Commary Statistics
Sequencing vector: plasmid;
Assembly program: Phrapy version 0.990329
Consensus quality: 200661 bases at least Q40
Consensus quality: 200661 bases at least Q20
Consensus quality: 200661 bases at least Q20
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NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces consists of 62 contigs. The true order of the pieces arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                          Submitted (18-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA On Mar 18, 2003 this sequence version replaced gi:28975751.
                                                                                                                  Submitted (17-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA (bases 1 to 214038)
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1621: gap of unknown length
2732: contig of 1111 bp in length
2832: gap of unknown length
4031: contig of 1119 bp in length
4031: contig of 1199 bp in length
4131: gap of unknown length
5844: contig of 1353 bp in length
6620: contig of 1353 bp in length
6720: gap of unknown length
6730: gap of unknown length
7842: contig of 1122 bp in length
7842: contig of 1002 bp in length
8944: contig of 1002 bp in length
10120: contig of 1007 bp in length
10120: contig of 1007 bp in length
10120: contig of 1007 bp in length
10120: gap of unknown length
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                                               Unpublished
2 ~ (bases 1 to 214038)
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                                                                                               Worley, K.C.
Direct Submission
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Butcow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wans, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ugdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morennon, K.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Halton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCU42674 1790 bp mRNA linear PRI 03-FEB-2004
Homo sapiens phospholipase B1, mRNA (cDNA clone MGC:35447
IMMGE:5191712), complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1790)
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Direct Submission
Submitted (12-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                            367 ITTITICICITAGAAIGAGCCCTICCTGAGAACCCCTCGGAAIAGIAACIACCCCC
                                                                                                                                                                                                                                                                                                                                                                                                               TGTCCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC
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Tissue Procurement: Life Technologies, Inc.
CDN Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                       Length 265;
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Pred. No. 2.9e-09;
0; Mismatches 5; Indels
        Regulation of human phospholipase-like enzyme Patent: WO 0231161-A 6 18-APR-2002; BAYER AG (DE)
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Contact: MGC help desk

    .265
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                                                                                       Location/Qualifiers
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7.4%;
Best Local Similarity 93.6%;
Matches 73; Conservative (
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AX417822.1 GI:21522940
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DEFINITION ACCESSION VERSION KEYWORDS

RESULT 5 AX417822 ORGANISM

REFERENCE AUTHORS

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Patent: WO 02062977-A 1 15-AUG-2002;
PE Corporation (NY) (US)
Location/Qualifiers
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Sequence 1 from Patent WO0231161.
AX417817
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NLEKENPYLLEFIGFSTSTWEGTAGLNVAALGGRANDILGEELPRAFVNVUSV
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MELASLYGGGGGCGACAMLAAQNNCTCLFHSOSBLEKOELKKVNWNLUGHGISSFSYWHQY
TOREDFAVVVQPFFONTLTPLARRGDTDLTFFSEDCFHFSDRGHAEVALALMNNLEF
TOREDFAVTSNNFTHSRAALKCFSPSSPYLYTLRNSRLLPDQAEEAPEVLYWAVPVAAGVG
LVVGIIGTVWRCRRGGRREDPPMSLRTYAL"
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                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Seriee: IRAK Plate: 50 Row: k Column: 10.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
     Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: ang@bcm.tmc.edu.
Guntact: ang@bcm.tmc.edu.
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                      /tissue_type="Brain, adult, 6 pooled whole brains"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yan,C., Ketchum,K., di Francesco,V. and Beasley,E.M. Human phospholipase b-like polypeptide and uses thereof
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93.6%; Pred. No. 3.6e-09;
tive 0; Mismatches 5; Indels
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/gene="PLBI"
/note="Lipase GDSL; Region: GDSL-like
Lipase/Acylbydrolase"
/db_xref="CDD:pfam00657"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein id="AAH42674.1"
db_xref="GI:27503749"
                                                                                                                                                                                                                 /organism="Homo sapiens"
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'product="PLB1 protein"
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/gene="PLB1"
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Best Local Similarity
Matches 73; Conserv
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AX711962
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PAT 26-SEP-2002
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                   367 TITITCTCTTAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 426
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human lipase and polynucleotides encoding the same
Patent: WO 02059328-A 1 01-AUG-2002;
   Length 1835;
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7.4%; Score 70; DB 6; Length 364
Best Local Similarity 93.6%; Pred. No. 3.9e-09;
Matches 73; Conservative 0; Mismatches 5; Indels
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Score 70; DB 6; Length 183
Pred. No. 3.6e-09;
0; Mismatches 5; Indels
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Patent: WO 0231161-A 1 18-APR-2002;
BAYER AG (DE)
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1. 3648
1. 3648="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX492941 4377 bp
Sequence 1 from Patent WO02059328.
AX492941
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Patent: WO 0231161-A 5 18-APR-2002;
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Direct Submission
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                  BAYER AG (DE)
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D63648
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Pred. No. 2.8e-08;
iive 0; Mismatches 0; Indels
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Regulation of human phospholipase-like enzyme
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Best Local Similarity 93.6%; Pred. No. 3.9e-09;
Matches 73; Conservative 0; Mismatches 5;
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PE Corporation (NY) (US)
Location/Qualifiers
1. .1776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                  Sequence 1925 from Patent W002068579.
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Sequence 5 from Patent WO0231161.
AX417821
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LEXICON GENETICS INC (US)
Location/Qualifiers
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Best Local Similarity 100.
Matches 67; Conservative
                             . .4377
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AX417821
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A590 bp mRNA linear ROD 01-NOV-2000 D63648 Complete cds. D63848.1 GI:2696235 phospholipase B. Ratrus nom-
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NPELDPEKDWKLITVLFSNTSQCHLCSSDQORRHLMGHMENLSGYLDYLHREVPRAFV
NUDLSEVLTWAQQHQETGFSPAPEICKCSETIKLSKAWQMSYQBAWEDLLASSKF
NKHETFRAVVOGSPESEVELPLERPSPODSTTALRINSWMEPVGRKDGTLMSEAEKT
MKCPSQESPYLFTYRNSNYQARQLKPIGKFQMKEGTKFTCPDKDPSDSIPTTVHRLRP
ADIKVIGAMGDSLTAGNGAGSSPGNYLDVLTQYRGLSMSVGGDFIETVTTLANILRE
FNPSLKGFSVGTGKFNTASSNYQAKGGKSDGLAAQAKKLVSLMKDDKTINPQEDWK
ITTVFTGGNDLGGSCNNLARFSPQTFTDNIKTALDILHAEVPRAFVNNVSVIETTPLIL
ELFNEFKVSCPRMILRSLCFCVLNLGENSABLAQUVERNRQYQEBTGKLIESGRXDTR
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NFSFPCKPKKLELSVLSKSVHSLRPSDIKLVAAIGNLETPPAFGSGVVNMEKPQSLES
                                                                                                                                                                                                                                                                                                                                                                              475 TGTCCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAAGAACTACACGTACCCC 534
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Location/Qualifiers
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Identification of functional domains of rat intestinal phospholipase B/lipase. Its cDNA cloning, expression, and tissue
                                                                                                                                                                                                                                                                                                                                             367 ITTTTCTCTTAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC
                                                                                                                                                                                                                                                                                     Gaps
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Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosto
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                       Length 608;
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36. .4388
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 ATCAAGCCAGCCATTGAG 444
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ELUCITA VULGENTENA VMPRILLEGLEJUSSE FAPUCERITUM KITHAKSAR ALMINKMILE VÜĞK
KTRHQNYRALGINGI SPELSTKUNSULGHGTSMS CEEKAPSASPPS GYHTLARPA
DIQVYAALGIDSVTAGNGI SEGGEGLADVTTQTRGLSYSAGGDRFLENYTTENI LIRBE
DIQVYAALGIDSVTAGNGI SEGGEGLADVTTQTRGLSYSAGGDRFLENYTTENI LIRBE
DIQVYAALGIDSVTAGNGI SEGGEGLADVTTQTRGLSYSAGGDRFLENYTTENI LIRBE
ITVMIGASDLOLOFOKUSONRYSANNESDHLINALDILLHKEEVPRALINIVDFRANFSI IRB
VPLKAPDKCEPUNGTSVLCUVUTPGEDSHELARLERAFTSKSYGSSMLQLVESGRYDTRE
DYLKAPDKELI ALACPTKOKPLETE TRNSKYTY DI KRA IENWGSDFLCTEGSPSKYPT
SVHELREPSDI KVVAANGETTTATGRRESESSEDTTWRGLSWSIGGGGTLETHTTLP
SVHELREPSDI KVVAANGETTTATGRRESESSSEDTTWRGLSWSIGGGGTLETHTTLP
SVHELREPSDI KVVAANGETTTATGRREGRAQDMLKKKKKSTFTINI QED
NILKKEPRESILGPSTGTLENTAGLNVAEGGARAQDMLKKKKKSTFTINI QED
SVLILGGRACLANFLAQURKSTREVYKT QHALDI FYBELPRYFINVVEYMELSG
LLHDQGGKCANPLAQVORGSCLKRSQNLMAMQELKKVNGNLDFRYFINVVEYMELSG
PRAVTVQPF FRUYTVVETKRSQNLMAMQELKKVNGNLDFRANALBANNMLEPVGKK
DPAVTVQPF FRUYTVVETKRSQNLMAMQELKKVNGNLLDRAKANNTLYMAVPVAAVGGLVVG
TITSMNTADVARVANGTVORT
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Cavia porcellus phospholipase B (PLB) mRNA, complete cds.
AF045454 AF04541 GI:3172336
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Delagebeaudeuf, C., Gassama-Diagne, A., Nauze, M., Ragab, A., Li, R.Y., Capdevielle, J., Ferrara, P., Fauvel, J. and Chap, H.
Direct Submission
Submitted (30-JAN-1998) INSERM unite 326, Hopital Purpan, Toulouse 31059, France
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

1 (bases 1 to 4608)

Delagebeaudeuf, C., Gassama-Diagne, A., Nauze, M., Ragab, A., Li, R.Y., Cagdevielle, J., Errara, P., Fauvel, J. and Chap, H.

Ectopic epididymal expression of guinea pig intestinal

phospholipase B. Possible role in sperm maturation and activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3170 CACCAAGGACAAGCCCTTCCTGAGAACCTTCCGGAACAGTAACTACAGGACCATATCAA 3229
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DPTVVLQPMFENVVMPRTLEGLPDSSFFAPDCFHFNVKTHARSAIALWKNMLEPVGR
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Pred. No. 8.6e-05;
0; Mismatches 11; Indels 0;
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J. Biol. Chem. 273 (22), 13407-13414 (1998)
98256256
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| Organism="Cavia porcellus" |
| Organism="Cavia porcellus" |
| Mol type="RNA" |
| db xref="taxon:10141" |
| tissue type="intestine" |
| tissue type="intestine" |
| 4608 |
| qene="PLB" |
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| qene="PLB" |
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product="phospholipase_B"
protein_id="AAC40129.1"
/db_xref="G1:3172337"
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32; Conservative (
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EVVAMPRWHQCTWLSKE'S EVACGESSE'TSLUI V VVWWAN TOER TRALLENGESSET ERRENGES

PAVVEOPE FYEVES EVACGESSE'TELSIUMYMWREVOGOKDEPEST ERRENGES

PAVVEOPE FYEVES EVEREPRODITLAISIUMYMWREVOGOKDEPEST ERRENGES

OBSPYLETYRISNYOSRILEKROROHEREGTE I KOEDKOD SOSTPT SVHELK PADI I KV

OBSPYLETYRISNYOSRILEKROROHEREGTE I KOEDKOD SOSTPT SVHELK PADI I KV

I GALGDS LTAGNGAGSREGHIJDVLTEYRGLISN'S TGADHYI SSYTTAP BNILERE FNPSL

I GALGDS LTAGNGAGSREGHIJDVLTEYRGLISN'S TGADHYOS THE BERNYL I TVV

SRVSCPRILIRN'C CRO'LLEDDNSTELEGILD NIKKYORTHOR I SEGRY TYRED FTV

VLOP FREKOD FYTS BEGLEDNY SPEAD CHER'S SKTHARAASALMYNMLEBYWGOKTTON

NENS ID I I CPNOAP FPLISTYROG I BGHGTWLT CRERT PSAS P PTS VHALRED FTV

AALGDS LTAGGGI GGSRCPOLADVI TOYRGLES'S SCGGGGSLANVYTI-LIN I ILBRE FNSULT

GYANGTODASNTNAFINGAV PCAKABELMSOVKTI, VOKMKOD PRINGED FNV

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EVVAMPRWHQGTMLSRPSPEACGCSGETSKLDTVVMQWSYQETWDSLLASSSPNDQES
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 CTCTTAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCCATCAA
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CLZNIS/109,C07H21/04,C07K14/47,C12NS/10,C12N9/16, PC
3/201/A61K38/46,
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1 (bases 1 to 4613)
1 (bases 1 to 4613)
1 (100, Hand Hasegawa, A.
NEW PHOSHOLIPASE AND DNA CODING THE SAME PATENT: JP 1997248130-A 1 22-SEP-1997;
TOJO HIROMASA, TONEN CORPOS Rattus SP. (rat)
PN JP 1997248190-A/1
PP 12-MRR-1996 JP 1996086022
PF 15-MRR-1996 JP 1996086022
PI TOJO HIROMASA, HASEGAMA AKIRA
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/tissue_type='ileum'
36. .4397
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Pred. No. 8.6e-05;
0; Mismatches 11;
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Rat mRNA for phospholipase.
E13935
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JP 1997248190-A/1.
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Matches 62;
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Boll,W., Schmid-Chanda,T., Semenza,G. and Mantei,N.
Messenger RNAs expressed in intestine of adult but not baby
rabbits. Isolation of cognate cDNAs and characterization of a novel
brush border protein with esterase and phospholipase activity
93.286138
                                                                                                                                                                                                                                                                                                                                                                                   3170 CACCAAGGACAAGCCCTTCCTGAGAACCTTCCGGAACAGTAACTACACGTACCCTATCAA 3229
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ACMGVVTVLSDIIGRFSPSALMPLCPETRLVPRGGAEDLWMQATELVRSMRENPQLDF
EHDWKLINVPFSNTSQCFPCPSAQQKGLVLGGMDKLTRTLDYLQQEVPKAFVNLVDLS
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AVVFQPFFYESSLSALLAEPPLQDPTTLALSLWNRWMEPIGRKEEPFSEKERKPLRCP
TQESPYLFTYRNSGQLTRVSQPQGKLEVREGTEIRCPDKDPSDSVPTSVHRLKPADIK
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/db_xref="UniProt/Swiss-Prot: Q05017"
/translation="MALWPSVFLLGLLPLLGRGADQIQTSSGKNTLEGQLWPESLKTF
                                                                                                                                                                                                                                                                                                                                               372 CTCTTAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCCATCAA 431
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-JUN-1992) WERNER BOLL, Dept. of Biochemistry 11, Swiss Federal Institute of, Technology, ETH Zentrum, Universitaetsstrasse 16, Zuerich, CH-8092, Switzerland Location/Qualifiers
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/product='phospholipase precursor'
36. .125
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84.9%; Pred. No. 8.6e-05;
ive 0; Mismatches 11; Indels
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                                                             peptide 126. .4394
/product='phospholipase'
Location/Qualifiers
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GASDLLCYCTDSNILYSAAMFYDHLABALDALHREVPRALVNIUVDFWNBSVTRQVPLG

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LQGFSVGTGRETTSQAFFNQAVAGARADGLIPQAQRLVALMKNDTRINFOEDWKIITV FIGGNDLCDFCNDPYRYSPONFTDNIGTALDILHAEIPRAFVNLVKVLEISKLRELYQ ETVSCPRHILRSLCPCVLKFDDNSTFIASLIETIKEYQERFYQLIDSGRYDTRDBFT VLLOFFERVANMPKTORIDSGRYDTRDBFT FOR THE SYGAHAHAASALMNNMLEPVGCKTTH NDFEGAFFEKVNMPKTOFTSYKNSVQGFGTWLPCRRSSPSASPFTSYHALRADIGUGNSTUTAGDSGRYDTBOTGVRGDSSTTGYRGLSYSSGGDGSLDNVTTLPNILRQFNSNL
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NFTYSRTKLKCPSPDSPYLYTLRNSRLLPDQARADPTVLYMAVPVAAAGAGLLGTLAN
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ALIGNMENTS

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gendard name= "single nucleotide polymorphism (SNP)"
splace(1406,A)
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grandard_name= "single nucleotide polymorphism (SNP)"
epiace(12926,A)
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gtandard name= "single nucleotide polymorphism
eplace(23007,A)
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standard name= "single nucleotide polymorphism
eplace(22401,C)
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'number= 8
replace(19708,C)
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replace(26490,G)
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23350. 24668
/*tag= ay
/number= 9
24669. 24749
/*tag= az
/*tag= az
24750. 26803
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            *tag= ae
strandard name= "single nucleotide polymorphism (SNP)"
strandard name= "single nucleotide polymorphism (SNP)"
strang= af
number= 4
[6399]. 16891
number= 4
number= 4
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standard_name= "single nucleotide polymorphism (SNP)"
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eplace(13964,G)
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standard_name= "single nucleotide polymorphism (SNP)"
splace(14087,A)
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standard_name= "single nucleotide polymorphism (SNP)"
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number= 3
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eplace(10473. .10474,T)
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|eplace(12159,A)
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'standard_name= "single nucleotide polymorphism (SNP)"
| standard_name= "single nucleotide polymorphism (SNP)"
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standard_name= "single nucleotide polymorphism (SNP)"
eplace(9859,G)
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eplace(9875,G)
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gplace(10279,T)
                                                                                                                                                                     "single nucleotide polymorphism (SNP)"
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ceplace(4924,G)
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The present invention relates to novel human phospholipase-like enzymes and polynucleotides encoding such proteins. Sequences of the invention are useful for producing a medicament for modulating the activity of phospholipase in a disease such as cancer, inflammation, cardiovascular disorders, chronic obstructive pulmonary diseases, central nervous system (CNS) disoracers such as brain injuries, cerebrovascular disease, dementia (Alzheimer's disease, Parkinson's disease, corticobasal degeneration, motor neuron disease, Pick's disease, Huntington's disease, Creutzfeld Jacob dementia, schizophrenia with dementia, korsakoff's psychosis, pain associated with CNS (e.g. epilepsy, failed back surgery syndrome, sciatica), multiple sclerosis, stroke, age associated memory impairment, allergic disease including asthma, allergic rhinitis (hay fever), atopic dermatitis, anaphylaxis and inflammation, cardiovascular disease, coronic obstructive pulmonary disease, acute respiratory distress syndrome, gout,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human phospholipase-like enzyme polypeptide useful for screening agents, and in the treatment of cancer, inflammation, diabetes, obesity, a central nervous system disorder, or a cardiovascular disorder.
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100.0%; Pred. No. 6.7e-290;
tive 0; Mismatches 0;
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13041 GGAAGTGGAGGCACGTTGTTCATGTTCCTGTGGGCCCCTAGGCCTTGTTTGGTTCAAGTC 13100
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    900
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26-DEC-2000; 2000US-0257293P.
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18-AUG-2000; 2000US-0226679F.
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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; 88.
                                                                                                                                                                                                                                                              91 TGTCCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACACGTTCC 150
                                                                                                                                                                                                                                          TTTTCTCTTAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 426
diabetes, emphysema or obesity. They are also used for treating anorexia, overweight, cachexia, bulimia, hypertension, type-II diabetes, coronary artery disease, hyperlipidaemia, gall bladder disease, osteoarthritis, sleep apnoea and respiratory problems, cancer (e.g. breast, prostate, colon cancer), thrombolytic disease, reduced fertility, polycystic ovarian syndrome, complications of pregnancy, menstrual irregularity, hirsublance, complications of pregnancy, menstrual irregularity, hirsublance, incontinence and depression. The present sequence is human phospholipase like enzyme encoding DNA
                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human reproductive system related antigen cDNA SEQ ID NO: 1391.
                                                                                                                                                                               Score 70; DB 6; Length 265;
Pred. No. 2.4e-11;
0; Mismatches 5; Indels
                                                                                                                                                  Sequence 265 BP; 73 A; 80 C; 62 G; 50 T; 0 U; 0 Other;
                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0190076P.
2000US-0198123P.
2000US-0209467P.
2000US-021515P.
2000US-021515F.
2000US-021515F.
2000US-021648P.
2000US-021648P.
2000US-021748P.
2000US-021748P.
2000US-021748P.
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14-AUG-2000; 2000US-0225447P-
14-AUG-2000; 2000US-0225757P-
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                                                                                                                                                                                  7.4%;
Best Local Similarity 93.6%;
Matches 73; Conservative (
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Human; testicular antigen; testes; cancer; metastasis; immune disorder
reproductive system disorder; urinary system disorder; gene therapy;
cardiovascular disorder; respiratory disorder; neurological disorder;
gastrointestinal disease; infection; cytostatic; gene; ss.
                                                                                    Human testicular antigen encoding cDNA SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US - 0225267P
2000US - 0225268P
2000US - 022540P
2000US - 0225447P
2000US - 0225758P
2000US - 0225758P
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2000US-0232397P
2000US-0232398P
                                           (first entry)
                                                                                                                                                                                                                                                                                     WO200155317-A2.
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                                           21-JUN-2002
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ABL96843;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4%; Score 70; DB 4; Length 572; llarity 93.6%; Pred. No. 3.7e-11; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Barash SC, Ruben SM;
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                             08 NOV-2000; 2000US-0246613F.
17-NOV-2000; 2000US-0246613F.
17-NOV-2000; 2000US-0249209F.
17-NOV-2000; 2000US-0249210F.
17-NOV-2000; 2000US-0249210F.
17-NOV-2000; 2000US-0249213F.
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17-NOV-2000; 2000US-0249213F.
17-NOV-2000; 2000US-0249218F.
17-NOV-2000; 2000US-0249218F.
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17-NOV-2000; 2000US-0249218F.
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17-NOV-2000; 2000US-024929F.
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17-NOV-2000; 2000US-02249299F.
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17-NOV-2000; 2000US-02299F.
17-NOV-2000; 2000US-02299F.
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17-NOV-2000; 2000US-02299F.
17-NOV-2000; 2
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2000US-0251990P.
2000US-0254097P.
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P-PSDB; AAM95420.
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les 73; Conserv
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05-JAN-2001;
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Best Loc Matches

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ABL96843 ID ABL9 XX RESULT

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20-OCT - 2000; 2000US-0241809P
20-OCT - 2000; 2000US-0241826P
01-NOV-2000; 2000US-0246414P
08-NOV-2000; 2000US-0246414P
08-NOV-2000; 2000US-0246414P
08-NOV-2000; 2000US-0246475P
08-NOV-2000; 2000US-0246477P
08-NOV-2000; 2000US-0246477P
08-NOV-2000; 2000US-0246478P
08-NOV-2000; 2000US-0246523P
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2000US-0249213P.
2000US-0249214P.
2000US-0249215P.
2000US-0249210P.
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2000US-0249210P.
2000US-0249218P.
                                                                                                                                                                  29-5EP-2000; 2000US-0255051.
29-5EP-2000; 2000US-0256802P.
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02-0CT-2000; 2000US-023703P.
02-0CT-2000; 2000US-023703P.
13-0CT-2000; 2000US-0239935P.
13-0CT-2000; 2000US-0239935P.
20-0CT-2000; 2000US-0239935P.
20-0CT-2000; 2000US-024966P.
20-0CT-2000; 2000US-024056P.
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2000US-0246525P.
2000US-0246226P.
2000US-0246527P.
2000US-0246528P.
                                                                             25-SEP-2000; 2000US-0234997P.
25-SEP-2000; 2000US-0234998P.
27-SEP-2000; 2000US-023834P.
27-SEP-2000; 2000US-023834P.
27-SEP-2000; 2000US-023837P.
29-SEP-2000; 2000US-023636P.
29-SEP-2000; 2000US-023636P.
29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236368P.
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2000US-0251988P
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2000US-0246610P.
2000US-0246611P.
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20-OCT-2000; 2000US-0241787P.
20-OCT-2000; 2000US-0241808P.
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20-OCT-2000;
20-OCT-2000;
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17-NOV-2000;
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                  14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
21-SEP-2000; 2
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KW antinfilanmatory; antirheumatic; antiarthritic; immunodeficiency virus; wantinfilanmatory; antirheumatic; antiarthritic; immunosuppressive; antinflammatory; antirheumatic; antiarthritic; immunosuppressive; wantibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; vulnezary; antiulcer; osteopathic; eczema; wantialtery; untimatary; antiulcer; osteopathic; eczema; wantialtery; antidatery; antidabetic; cytostatic; when recorrective; antidepressant; nootropic; antipabetic; cytostatic; wantimnostimunant; one therapy; antisense therapy; vaccine; inflammation; wantianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; wantianaphylactic; rheumatoid arthritis; platelet disorder; asthma; we cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; wanterpatic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; wallergic rhinitis; diabetes; multiple sclerosis; depression; wallergic anaphylactic; antides and allergic chinitis; diabetes; multiple sclerosis; depression; wallergic antider; parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 TITICICITAGAATGAGCCCTTCCTGAGAACCCCTGGGAATAGTAACTACACGTACCCC 426
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                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a cDNA of the
                                                                                                                                                                                                                                                                                                             Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 572 BP; 146 A; 159 C; 157 G; 106 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human protein encoding cDNA sequence SEQ ID NO:600.
                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 511; 766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH99765 standard; cDNA; 802 BP.
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                                                                                                                                                                                                                                                Barash SC, Ruben SM;
05-DEC-2000; 2000US-025419P.
06-DEC-2000; 2000US-025185P.
08-DEC-2000; 2000US-025185F.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-025199P.
11-DEC-2000; 2000US-025199P.
05-JAN-2001; 2001US-025499P.
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                                                                                                                                                                                                                                                    Rosen CA,
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neurological disorder; ss

WO200153455-A2 Homo sapiens

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AAM25963. The proteins can have activities based on the tissues and cells

AAM25963. The proteins can have activities based on the tissues and cells

they are expressed in such as: antibnflammatory; antirheumatic;

antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;

central nervous system; virucide; antibacterial; endocrine;

cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;

cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;

cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;

cardiovascular; antianaemic; antiaggregant; haemostatic; untiagregan;

cardiovascular; antianaemic; antiaggregant; nortidepressant; nocropic;

antidabetic; cytostatic; neuroprotective; antidepressant; nocropic;

antidatheric; oxtostatic; neuroprotective; antidepressant; nocropic;

antidatheric; cytostatic; neuroprotective; antidepressant; nocropic;

antidatheric; oxtostatic; neuroprotective; antidepressant; nocropic;

cardiovascular; antidepressant; neuroprotective; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressant; antidepressan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 TTTTTCTCTTAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 426
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                                                                                                                                                                                                                                                                                                                                                                                                            Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
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Pred. No. 4.5e-11;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 802 BP; 206 A; 236 C; 211 G; 149 T; 0 U; 0 Other;
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. 4.5e-11;
rches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 634; 1217pp; English.
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                                                                                                                                                   21-JAN-2000; 2000US-0048B725.
25-APR-2000; 2000US-00552317.
                                                                                                                                                                                                                                                                              Fang YT, Liu C, Drmanac RT;
                                                                           22-DEC-2000; 2000WO-US035017.
                                                                                                                              99US-00471275
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les 73; Conservative
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                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAM25824
                                                                                                                        23-DEC-1999;
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                          26-JUL-2001
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host calls comprising a cultivation also relates to vectors and recombinant host calls comprising a conclectide of the invention, methods of producing the nucleotides or polypeptides in a sample, and methods of identifying compounds which compared to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities, sem cell growth factor activity; is memberedic or chemokinetic activity; tissue growth activity; and the invention are useful cativity; activin- or inhibin-related activities, chemokinetic or chemokinetic activities, haematopolytic activities, considered activities, chemokolytic activities, considered activities, considered activities, conditions or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., metaling or lapinand and phornand conditions, e.g., by protein or gene therapy. Such conditions included arterial ischaemia, bone disorders (e.g., metaling or lapinand and protein or gene therapy. Such conditions and conditions, e.g., by protein or gene therapy. Such conditions are useful growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promoce wound repair (or nucleic acids encoding them) may be used in che conditions of the aling (e.g., of burns, incisions and ulcers), while those with any place of promoce call growth. For example, such polypeptides may be used in cell cultures to promoce cell growth. For example, such polypeptides may be used in the incast of a such and a c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nan proteins and DNA encoding sequences useful for preventing, treating ameliorating a medical condition in a mammalian subject e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a
chronic inflammatory condition, proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; beteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiniflammatory; antiaethmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 365; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-2001; 2001WO-US003800.
                                                                                                                                                                                                                                                                                                                                                                                                                                03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Liu C, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                              WO200157188-A2.
                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        novel
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Sequence 802 BP; 206 A; 236 C; 211 G; 149 T; 0 U; 0 Other;

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Gaps

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ABQ82234;

ABQ8223

ð 8

S'UTR

CDS

3'UTR

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KW. Human; phospholipase-like enzyme; cancer; inflammation; Pick's disease; KW. eardiovascular diseace; central nervous system disorder; brain injury; cardiovascular disease; dementia; KW. direnier's disease; Parkinson's disease; corticobasal degeneration; M. Alzheimer's disease; Parkinson's disease; corticobasal degeneration; KW. Alzheimer's disease; Huntington's disease; Creutzfeld Jacob dementia; M. motor neuron disease; Huntington's disease; pain; papilepsy; multiple sclerosis; KW. sciatica; stroke; age associated memory impairment; allergy; asthma; allergic rhinitis; hay fever; acopic dermatitis; cardiovascular disease; Allergic rhinitis; hay fever; acopic dermatitis; cardiovascular disease; chronic obstructive pulmonary disease; emphysema; obesity; anorexia; chromic obstructive pulmonary disease; emphysema; obesity; anorexia; chromic obstructive pulmonary disease; emphysema; obesity; anorexia; chromic obstructive pulmonary disease; emphysema; obesity; disease; symporalipidaemia; gall biadder disease; osteoarthritis; got, sleep apnoea; respiratory problem; polycystic ovarian syndrome; thrombolyvic disease; reduced fertility; pregnancy; stress incontinence; whirsutism; menstrual irregularity; depression; enzyme; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human phospholipase-like enzyme polypeptide useful for screening agents, and in the treatment of cancer, inflammation, diabetes, obesity, a central nervous system disorder, or a cardiovascular disorder.
                                                                                                                                                                                                    367 TTTTCTCTAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Human phospholipase-like enzyme"
/product= "Human phospholipase-like enzyme"
/note= "CDS does not include start and stop codon"
                                   Sequence 1835 BP; 458 A; 549 C; 474 G; 354 T; 0 U; 0 Other;
                                                                                  Length 1835;
                                                                                  ch 7.4%; Score 70; DB 6; Length 183
1 Similarity 93.6%; Pred. No. 7.1e-11;
73; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human phospholipase-like enzyme encoding CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD37410 standard; cDNA; 3648 BP.
                                                                                                                                                                                                                                                                                    427 ATCAAGCCAGCCATTGAG 444
                                                                                                                                                                                                                                                                                                             395 ATCAAGCCAGCCATTGAG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2000; 2000US-0238445P.
26-DEC-2000; 2000US-0257293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-OCT-2001; 2001WO-EP011641
prostate, colon or leukocytes
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                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD37410;
                                                                                                    Query Match
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                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human phospholipase protein (I) located on Chromosome 2. (I) can be used for identifying agents that modulate its chromosome 2. (I) can be used for identifying agents that modulate its coffunction or activity where the agent is useful for treating a disease or condition mediated by a the human phospholipase protein. (I) peptides can be used in substantial and specific assays related to functional cofficient of the peptide sequences, to raise antibodies or to elicit information of the peptide sequences, to raise antibodies or to elicit corresponding protein is assays that determine the levels of protein in biological fluids, and as markers for tissues where the corresponding protein is expressed. Nucleotide sequences encoding (I) can corresponding protein is expressed. Nucleotide sequences encoding (I) can corresponding protein. (I) and chemical intermediates in biological portions of the protein. (I) and nucleic acid molecules encoding it can be used in the identification of therapeutic and may serve as modulate phospholipase activity in cells and tissues that express the modulate phospholipase activity in cells and tissues that express the protein as in kidney, blood, lung, brain glioblastomas,
                                                                   ö
                                                                                                            367 TITITICICITAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human phospholipase proteins, useful for the development of human therapeutics and diagnostic compositions, drug screening assays, tissue typing and pharmacogenomic analysis.
                                                                                                                                          0; Gaps
                    Length 802;
                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human phospholipase protein encoding cDNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; phospholipase; enzyme; chromosome 2; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Di Francesco V, Beasley EM;
                         Query Match 7.4%; Score 70; DB 4; 1
Best Local Similarity 93.6%; Pred. No. 4.5e-11;
Matches 73; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
176 .1594
//tag= b
/product= "phospholipase"
1595 .1815
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    ABQ82234 standard; cDNA; 1835 BP.
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                                                                                                                                                                                                                                              255 ATCAAGCCAGCCATTGAG 272
                                                                                                                                                                                                                        427 ATCAAGCCAGCCATTGAG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001; 2001US-00778961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JAN-2002; 2002WO-US002302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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P-PSDB; ABP53556.
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Yan C,

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The present invention relates to novel human phospholipase-like enzymes and polynucleotides encoding such proteins. Sequences of the invention are useful for producing a medicament for modulating the activity of phospholipase in a disease such as cancer, inflammation, cardiovascular choospholipase in a disease such as cancer, inflammation, cardiovascular diseases, chronic obstructive pulmonary diseases, central nervous system (CNS) disorders such as brain influries, cerebrovascular disease, dementia (Alzheimer's disease,) Parkinson's disease, corticobasal degeneration, motor neuron disease, Pick's disease, Huntington's disease, Creutzfeld acobamentia, schizophrenia with dementia, Korsakoff's psychosis, pain associated with CNS (e.g. epilepsy, failed back surgery syndrome, callergic disease including asthma, allergic rhinitis (hay fever), atopic dermatitis, anaphylaxis and inflammation, cardiovascular disease, chronic obstructive pulmonary disease, acute respiratory distress syndrome, gout, cartery disease, hyperlipidaemia, gall bladder disease, osteoarthritis, artery disease, hyperlipidaemia, gall bladder disease, osteoarthritis, colon cancer), thrombolytic disease, reduced fertility, polycystic colon cancer), thrombolytic disease, reduced fertility, polycystic colon cancer), thrombolytic disease, reduced fertility, menstrual irregularity, human and human and depression. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2401 TGTCCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 2460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 ITITICECTIAGAATGAGCCCTICCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer; hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3648 BP; 899 A; 1032 C; 947 G; 770 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.4%; Score 70; DB 6; Length 3648; 93.6%; Pred. No. 1e-10; rative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     numan phospholipase like enzyme encoding cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABX97048 standard; cDNA; 4268 BP
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08-MAR-2001; 2001US-0274194P.
08-MAR-2001; 2001US-0274281P.
09-MAR-2001; 2001US-0274849P.
13-MAR-2001; 2001US-0275235P.
13-MAR-2001; 2001US-0275535P.
13-MAR-2001; 2001US-0275579P.
13-MAR-2001; 2001US-0275501P.
14-MAR-2001; 2001US-027600P.
16-MAR-2001; 2001US-027600P.
16-MAR-2001; 2001US-027600P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 93.6
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NOV24a cDNA
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2001US - 0277791P

2001US - 0277813P

2001US - 0278132P

2001US - 027899P

2001US - 0279344P

2001US - 0279344P

2001US - 0279348P

2001US - 0279338P

2001US - 0280802P

2001US - 0280802P

2001US - 0280802P

2001US - 028194P

2001US - 028194P

2001US - 028194P

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2001US - 0291485P

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2001US - 029489P

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2001US-0309198P.
2001US-0312903P.
2001US-0318462P.
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2001US-0333184P.
2001US-0333272P.
2001US-0332094P.
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2001US-0325430P.
2001US-0325681P.
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2001US-0338092P.
2001US-0337185P.
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                              22-MAR-2001;
23-MAR-2001;
26-MAR-2001;
                       21-MAR-2001;
                                                                             30-MAR-2001;
                                                                      28-MAR-2001;
                                                                                                     02-APR-2001;
                                                                                                                                     13-APR-2001;
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(CURA-) CURAGEN CORP.

Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
Estuturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;
Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;
Lepley DM, Rieger DK;

2002-723332/78. WPI; 2002-723332/7 P-PSDB; ABU65081.

NOVX polypeptides and polynucleotides, useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial

Claim 13; Page 167-168; 1103pp; English.

asthma

This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive

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The invention relates to 566 new isolated human polypeptides and their encoding genes, sequences that are at least 95% identical to these or sequences comprising one or more conservative substitutions in these. The sequences comprising one or more conservative substitutions in these. The polypeptide, polynucleotide and antibodies against the polypeptides are useful in diagnosing, treating or preventing NOVX associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, hatheimer's disease, asthma, or fertility disorders. Alzheimer's disease, asthma, or fertility disorders. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This sequence represents an example of the nucleic acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 979; 1503pp; English.
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ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; antiinfertility; ardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AID; multiple sclerosis; graft-versus-host disease; Alzheimer's disease; Parkinson's disease; asthma; fertility disorder; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; vaccine.
                                                                                                                                                                                                                                             3016 IGICCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 3075
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activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atheroscierosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABX97008-ABX97185 are cDNA fragments amplified and isolated by the PCR primers and probes represented in ABX13460-ABX1362 and ABX97186-ABX97185 encode the NOVX proteins described in
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                                                                                                                                            Sequence 4268 BP; 1039 A; 1209 C; 1119 G; 901 T; 0 U; 0 Other;
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2002US-0385615P.
2002US-0385755P.
2002US-0386355P.
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2002US-0386447P.
2002US-0386447P.
2002US-0386465P.
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11-JUN-2002; 2002US-0387610P.
11-JUN-2002; 2002US-0387659P.
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11 M, Edinger SR;
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09-AUG-2002; 2002US-0401628P.
13-AUG-2002; 2002US-0402822P.
13-AUG-2002; 2002US-0403422P.
15-AUG-2002; 2002US-0403412P.
15-AUG-2002; 2002US-0403732P.
25-AUG-2002; 2002US-0406182P.
12-SEP-2002; 2002US-0410585P.
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30-SEP-2002; 2002US-0415955P.
11-JUN-2002; 2002US-0387668P.
11-JUN-2002; 2002US-0387696P.
12-JUN-2002; 2002US-0387994P.
12-JUN-2002; 2002US-0387994P.
12-JUN-2002; 2002US-0387966P.
12-JUN-2002; 2002US-0388432P.
12-JUN-2002; 2002US-0388432P.
12-JUN-2002; 2002US-0388432P.
13-JUN-2002; 2002US-038943P.
14-JUN-2002; 2002US-0389146P.
17-JUN-2002; 2002US-0389146P.
17-JUN-2002; 2002US-0389148P.
18-JUN-2002; 2002US-0389148P.
19-JUN-2002; 2002US-0389144P.
19-JUN-2002; 2002US-0399064P.
19-JUN-2002; 2002US-0390068P.
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19-JUN-2002; 2002US-0390068P.
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05-NOV-2002; 2002US-0423748P.
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New NOVX polypeptides and nucleic acid molecules useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or
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Patturajan M,
Fernandes ER,
                                31-MAY-2001; 2
31-MAY-2001; 2
118-JUN-2001; 2
119-JUN-2001; 2
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12-SEP-2001;
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  3016 TGTCCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 3075
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                                                                                                                                                                                                                                                                          Human; 88; gene; NOVX; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease.
                                            Gaps
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Sequence 4268 BP; 1039 A; 1209 C; 1119 G; 901 T; 0 U; 0 Other;
                      Length 4268;
                    7.4%; Score 70; DB 12; Length 42 93.6%; Pred. No. 1.1e-10; ative 0; Mismatches 5; Indels
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19-MAR - 2001; 20010S - 0274849P.
113-MAR - 2001; 20010S - 027523P.
113-MAR - 2001; 20010S - 027553P.
113-MAR - 2001; 20010S - 0275579P.
113-MAR - 2001; 20010S - 0275579P.
113-MAR - 2001; 20010S - 027601P.
14 MAR - 2001; 20010S - 027694P.
20 MAR - 2001; 20010S - 027733P.
20 MAR - 2001; 20010S - 027733P.
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21 MAR - 2001; 20010S - 027733P.
22 MAR - 2001; 20010S - 027733P.
23 MAR - 2001; 20010S - 027733P.
24 MAR - 2001; 20010S - 027733P.
25 MAR - 2001; 20010S - 027733P.
27 MAR - 2001; 20010S - 027899P.
27 MAR - 2001; 20010S - 027899P.
27 MAR - 2001; 20010S - 027899P.
28 MAR - 2001; 20010S - 027899P.
29 MAR - 2001; 20010S - 027899P.
20 MAR - 2001; 20010S - 027999SP.
30 MAR - 2001; 20010S - 028989E.
30 MAR - 2001; 20010S - 028989E.
31 MAR - 2001; 20010S - 028989E.
31 MAR - 2001; 20010S - 028989E.
31 MAR - 2001; 20010S - 028989E.
32 MAR - 2001; 20010S - 028989E.
33 MAR - 2001; 20010S - 028989E.
34 MAR - 2001; 20010S - 028989E.
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36 MAR - 2001; 20010S - 028989E.
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03-MAY-2001; 2001US-0288528P.
15-MAY-2001; 2001US-0291190P.
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                                                                                                                                                                                                                                                       Human cDNA encoding NOV24a.
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                  Query Match 7.4
Best Local Similarity 93.6
Matches 73; Conservative
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Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li I Gusev VY, Ji W, Gorman L, Miller CE, Kekuda R, M Gangolli EA, Vernet CAM, Guo XS, Tchernev VT, R, Cseman SJ, Malyankar UM, Gerlach V, Liu Y, Spaderna SK, Catterton E, Leite MW, Zhong H; P, Lepley DM, Rieger DK, Burgess CE;
2001US-0294899

2001US-0299027P

2001US-0299037P

2001US-029910P

2001US-039434P

2001US-0318462P

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TCHERNEV V T.
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MALYANKAR U M.
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                                                                                           The invention relates to an isolated polypeptide (designated NOVX, or NOV127) comprising a sequence selected from 178 fully defined amino acid sequences (and their mature forms, variants and fragments). Also acid sequences (and their mature forms, variants and fragments). Also acid sequences (and their mature forms, variants and fragments). Also comprising the nucleic acid, a cell comprising the vector, methods for comprising the presence or amount of the polypeptide or the nucleic acid determining the presence of or amount of the polypeptide or the nucleic acid colecule in a sample, methods for determining the presence of or subject, a method for identifying an agent that binds to the above cuse in the treatment of a pathology that is related to aberrant or subject, a method for identifying a potential therapeutic agent for use in the treatment of a pathology that is related to aberrant or a pathology was not a modulation of activity or of latency or predisposition to acreening for a modulator of activity or of latency or predisposition to are useful for diagnosing, preventing or treating diseases such as are useful for diagnosing, preventing or treating diseases such as are useful for diagnosing, preventing or treating diseases or cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or parkinson's disease, immune disorders, heamtopoletic disorders, concer-associated in chromosome mapping, tissue typing, preventive medicine and chromosome mapping, tissue typing, preventive medicine and chromosome mapping, tissue typing, preventive medicine and chromosome mapping, the polypeptides are also useful as vaccines. The polypeptides are also useful as vaccines. The
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                                                                  Claim 17; SEQ ID NO 81; 786pp; English.
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17-MAY-2002; 2002US-0381558P.
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Best Local Similarity 93.0.
Local 73; Conservative
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                         pharmacogenomics
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This invention relates to novel human enzymes (ENZM) and the genes which encode them. The invention may be useful for the development of compounds with a cytostatic, antiarteriosclerotic, anticonvulsant, nootropic, with a cytostatic, antiarteriosclerotic, antianlergic, antiantlergic, antiantlergic, antiantlergic, antiantlergic, antiantlergic, antiantlergic, antiantlergic, control of the may therefore be useful in disquesting, treating and preventing invention may therefore be useful in disquesting, treating and preventing conversation of ENZM, such as cell proliferative (for example cancer, overexpression of ENZM, such as cell proliferative (for example cancer, atherosclerosis), neurological (for example plyplepy, mutington's conversation of ENZM, such as cell proliferative (for example AIDS, allergies) and developmental (for example Hypothyroidism, Cushing's syndrome) disorders or infections. These are also useful in assessing the effects of conformation the expression of mucleic acid and amino acid sequences of ENZM. The present sequence is that of a gene which encodes a conformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 TITICICITAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 426
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                                                                                                                                                                                                                                                                                                        New human enzymes (ENZM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant ENZM expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or infections.
Khare R, Kable AE, Lee SY, Hafalia AJA, Chawla NK, Marquis JP;
Ramkumar J, Wilson AD, Jin P, Hawkins PR, Bulloch SA, Swarnakar A;
Elliott VS, Richardson TW, Mason PM, Baughn MR, Yue H, Becha SD;
Tang YI, Batra S, Lu DAM, Bhatia UG, Burrill JD, Lee S, Blake JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70; DB 12; Length 4311;
Pred. No. 1.1e-10;
0; Mismatches 5; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "Human lipase NHL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lipase NHL (Ala 1318 variant) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; SEQ ID NO 86; 463pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Local Similarity 93.6%;
les 73; Conservative
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                                                                                                                                                                 Gao J;
                                                                                                                                                                                                                               WPI; 2004-053042/05.
                                                                                                          Tang YT, bac.
                                                                                                                                                                                                                                                                       P-PSDB; ADH13664.
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diagnostic reagent; clinical trial monitoring; cosmetic; nutriceutical; nuttation detection; gene expression analysis; transgenic animal; noctropic; cytostatic; antiinflammatory; single nucleotide polymorphism; SNP; gene therapy; gene; se.

clotting disorder; cancer; drug screening; mental disorder; NHL;

/*tag= b
/note= "Single nucleotide polymorphism (SNP); leads to a
Val to Ala substitution at position 1318 of the protein"

"Human lipase NHL

replace (3953, C)

variation

/*tag= a /product=

Location/Qualifiers

sapiens

Ношо Key

بعث

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The invention relates to a novel human lipase (NHL; ABB09555, ABB09556)
and to nucleic acids encoding it (ABQ77623, ABQ77624). The NHL has
construct al similarity with animal lipases, particularly phospholipase B.
Constructural similarity with animal lipases, particularly phospholipase B.
Construction with human thyroid and brain cDNAs. The NHL gene is
n conjunction with human thyroid and brain cDNAs. The NHL gene is
located on chromosome 2, and contains a C/T polymorphism at position 3953
of the open reading frame (ORF), resulting in an Ala/Val substitution at
constitution 1318 in the protein. NHL nucleotides and proteins are useful for
treating disorders such as inflammatory or proliferative disease,
infectious disease, clotting disorders, and cameer. They can also be used
in screening for compounds useful in the treatment of mental, biological
or medical disorders, as diagnostic reagents, in clinical trial
conflicting and in cosmetic and nutriceutical applications. NHL
conflictionally be used in the detection of disease.

associated mutations, in the analysis of gene expression, for the
therapy, and as part of ribozyme and/or triple helix sequences useful in
the modulation of NHL gene expression. The present sequence represents
conversed to the modulation of NHL sequence represents
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                    /*tag= b
/note= "Single nucleotide polymorphism (SNP); leads to an
Ala to Val substitution at position 1318 of the protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 TITITCICITAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 426
                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotides encoding human lipases that are structurally related to animal lipases, particularly phospholipase B, useful for drug screening, diagnosis and in gene therapy of biological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.4%; Score 70; DB 6; Length 4377;
13.6%; Pred. No. 1.1e-10;
.ve 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 36-37; 44pp; English.
  replace (3953, T)
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                                                                                                                                                                                 22-JAN-2002; 2002WO-US001715
                                                                                                                                                                                                                         24-JAN-2001; 2001US-0264049P
                                                                                                                                                                                                                                                            (LEXI-) LEXICON GENETICS INC.
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                                                                                                                                                                                                                                                                                                    Yu X, Miranda M,
                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ABB09555
                                                                                                  WO200259328-A1
                                                                                                                                         01-AUG-2002
variation
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Polynucleotides encoding human lipases that are structurally related to animal lipases, particularly phospholipase B, useful for drug screening, diagnosis and in gene therapy of biological disorders.

Turner CA;

Yu X,

2002-599797/64. Miranda M,

P-PSDB; ABB09556.

22-JAN-2002; 2002WO-US001715 24-JAN-2001; 2001US-0264049P (LEXI-) LEXICON GENETICS INC.

WO200259328-A1

01-AUG-2002

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The invention relates to a novel human lipase (NHL; ABB09555, ABB09556)

and to nucleic acids encoding it (ABQ77623, ABQ77624). The NHL has

Extructural similarity with animal lipases, particularly phospholipase B.

Computed sencoding NHL were obtained using human genomic sequences
in conjunction with human thyroid and brain cDNAs. The NHL gene is
confidention with human thyroid and brain cDNAs. The NHL gene is
confidention conjunction with human thyroid and brain cDNAs. The NHL gene is
confidential in the protein. NHL uncleotides and proteins are useful for
treating disorders such as inflammatory or proliferative disease,
confidential disorders, and cancer. They can also be used
infectious disease, clotting disorders, and cancer. They can also be used
in screening for compounds useful in the treatment of mental, biological
or medical disorders, as diagnostic reagents, in clinical trial
conficting and in cosmetic and nutriceutical applications. NHL
completides can additionally be used in the detection of disease.

Completides can additionally be used in the detection of disease.

Completides can additionally be used in the detection of disease.

Completides can additionally be used in the detection of disease.

Completides can additionally be used in the detection of the encoding the valuation of NHL gene expression. The present sequence represents

Completides can additionally wariant of NHL. Note: The present sequence is

Comblement to the modulation of the present sequence is

Comblement to the specification, but was derived from the the information of any and the present sequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 TTTTTCTCTTAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC
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0; Mismatches 5
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Conservative
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les 73; Conserv
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Matches
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Human; lipase; chromosome 2; phospholipase B homologue; thyroid; brain; inflammatory disease; proliferative disease; infectious disease;

Human lipase NHL (Val 1318 variant) cDNA.

(first entry)

21-OCT-2002

WPI; 2003-120797/11.

RESULT 15

3178 ATCAAGCCAGCCATTGAG 3195

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Yue H, Azimzai Y, Baughn MR, Burford N, Reddy R;
Das D, Nguyen DB, Yao MG, Arvizu CS, Lu Y, Gandhi AR;
A, Elliott VS, Ramkumar J, Lal PG, Lu DAM, Lee EA, Lee SY;
ang J, Tribouley CM, Kable AE, Swarnakar A;
                                                                                              Human; lipid-associated molecule; LIPAM; cardiovascular disorder; stroke; arteriovenous fistula; atheroscierosis; hypertension; Raynaud's disease; aneurysm; congestive heart failure; thrombophlehitis; andina pectoris; ischaemic heart disease; rheumatic heart disease; peptic oesophagitis; gastrointestinal disorder; lipid metabolism disorder; Crohn's disease; nausea; peptic ulcer; fatty liver; Rabry; disorder; Crohn's disease; dautoimmume disorder; linflammatory disorder; neurological disorder; kuru; acquired immunodeficiency syndrome; anamaia; Alzheimer; disorder; kuru; dementiai; prion disease; Creutzfeldt Jakob disease; leukaemia; cancer; adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; gene therapy; protein replacement therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Human mature LIPAM-9 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human mature LIPAM-9 protein"
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                                                                                                                                                                                                                                                                                                                                 "Human LIPAM-9 protein"
                                                                             Human lipid-associated molecule (LIPAM)-9 cDNA.
                                                                                                                                                                                                                                                                                          Location/Qualifiers
9. 2918
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Yue H, Azimzai Y, B
Walia NK, Das D, Nguyen DB,
Griffin JA, Elliott VS, Ramku
Yue H, Yang J, Tribouley CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-2001; 2001US-0293726P.
01-JUN-2001; 2001US-0293346P.
06-JUL-2001; 2001US-0303444P.
24-AUG-2001; 2001US-0314754P.
22-JAN-2002; 2002US-0351262P.
29-MAR-2002; 2002US-0368799P.
      AAD52634 standard; cDNA; 4424 BP
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9.65
/*tag= b
66.2915
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/product=
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/product= '
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                                   AAD52634;
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AAD52634
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The present invention relates to novel human lipid-associated molecules (LIPAM) and polynucleotides encoding such proteins. Sequences of the invention are useful for treating diseases or conditions associated with cereased expression of functional LIPAM. The antagonist is useful for treating a disease or condition associated with the overexpression of tunctional LIPAM. They are useful for diagnosing, treating or preventing cardiovascular disorders (e.g. arteriovanous fistula, arherosclerosis, cardiovascular disorders (e.g. arteriovanous fistula, arherosclerosis, cardiovascular disorders (e.g. peptic or rheumatic heart disease, aneuryms, varicose veins, congestive heart failure, thrombophlabitis, angina pectoris, ischaemic heart disease.

C esophagitis, anatea, peptic ulcer or Crohn's disease, disease, diabetes or inflammatory disorders (e.g. acquired immunodeficiency syndrome, cor inflammatory disorders (e.g. acquired immunodeficiency syndrome, cor inflammatory disorders (e.g. acquired immunodeficiency syndrome, cor creutzfeldt-asko disease), neurological disorders (e.g. stroke, anemia, asthma or Crohn's disease, or prion diseases such as kuru epilepsy, dementia, Alzheimer's disease, or prion diseases such as kuru epilepsy, dementia, myeloma or sarcoma). They are also used in gene therapy and protein replacement therapy. The present sequence is human corrected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2939 IGTCCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 2998
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                                                                      New human lipid-associated molecule (LIPAM) proteins and polynucleotides, useful for diagnosing, treating or preventing cardiovascular disorders (e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                         Claim 74; Page 168-169; 171pp; English.
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Job time : 496.725 secs
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nes 73; Conservative
                                         P-PSDB; AAE34448.
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Sequence 3 Sequence 3 Sequence 1

Sequence 155. App Sequence 15477, A Sequence 16433, A Sequence 17550, A Sequence 17550, A Sequence 12557, A Sequence 12577, A Sequence 12577, A Sequence 12577, A Sequence 12567, A Sequence 14568, A Sequence 14568, A Sequence 14568, A Sequence 14568, A Sequence 14568, A Sequence 14569, A

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Sequence 13611, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASSOCIATED
OF DETECTION AND USES THEREOF
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; Batent No. 6812339
; GENERAL INPORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS(
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF I
; TITLE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR PELING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
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US-09-949-016-13451

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US-09-940-016-16536

US-09-949-016-16473

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US-09-949-016-16473

US-09-949-016-1477

US-09-949-016-17550

US-09-949-016-17550

US-09-949-016-17560

US-09-949-016-12567

US-09-949-016-12567

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Best Local Similarity 55.2
Matches 79; Conservative
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Sequence 13611, A
Sequence 2163, Ap
Sequence 1767, Ap
Sequence 1777, Ap
Sequence 17305, A
Sequence 17305, A
Sequence 17305, A
Sequence 12697, A
Sequence 12617, A
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84673, A
15638, A
11852, A
14166, A
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15425, A
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13757, A
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Sequence 1767, Ap
Sequence 12896, Ap
Sequence 17305, A
Sequence 17305, A
Sequence 1731, A
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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Compugen Ltd.
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US-09-543-681A-1767

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US-09-949-016-12894

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US-09-949-016-12813

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3423, Ap 14676, A

Sequence Sequence

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Sequence 1767/c

Sequence 1767, Application US/09543681A

Sequence 1767, Application US/09543681A

Sequence 1767, Application US/09543681A

Sequence 1767, Application US/09543681A

Parent No. 6665709

GENERAL INFORMATION:
TITLE OF INVENTION: ULCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILLIATION OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT PELLORYION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 167

LENTH: 285
Sequence 16480, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WIMBER: 60/241,755
FRICK REPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 16480

LEAGTH: 225127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 TATGITIATACAGITCTTTCTATATAAGIGCAGAAGAATCATGITAAATAAATCIACAGG
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Best Local Similarity 53.8%; Pred. No. 0.033;
Matches 78; Conservative 0; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: misc_feature
LOCATION: (1)...(221127)
... OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.6%;
Matches 77; Conservative
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US-09-543-681A-1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
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US-09-543-681A-2163/C
US-09-543-681A-2163/C
Sequence 2163, Application US/09543681A
Sequence 2163, Application US/09543681A
Sequence 2163, Application US/09543681A
SEQUENCE 2163, Application US-09-09
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: UNCHER: US/09/543,681A
CURRENT PILING DATE: 2000-04-05
PRIOR PILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2163
LENGTH: 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 GCAGGAITGITAGITITICICCTICICAAGCAAACTICAGIGCTGICAGATAACTICICC 356
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Pred. No. 0.014;
0; Mismatches 66; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              4.3%; Score 40.6; DB 4;
55.2%; Pred. No. 0.21;
iive 0; Mismatches 64;
                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FEASTER 2000-09-08
SOPTWARE: FEASTER 2000-09-08
ILENGTH: 96074
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Best Local Similarity 54.5%;
Matches 79; Conservative
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; ORGANISM: Proteus mirabilis
US-09-543-681A-2163
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Best Local Similarity 55.2
Matches 79; Conservative
                                       FILE REFERENCE: CL001307
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US-09-949-016-16480/C
                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13611
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TITLE OF INVENTION: POLYMORENEEN, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: POLYMORENISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORENISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORENISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT PAPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
199 TACCTATCCTATTTTTTAAGAATACATTATTGACATCACTTTATTT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 WYYWMISRGSYRRYKISAMMGRAKMKRKKKIKKWYWMKGGGKKGGSIYM-AMRSRRGSIG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 ATTACAAAGCCAAGAAAATAGATAGGTCTGAGGATTAGGGGAGCTGTTCAGTTGCTAGGAG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 TTATACAGTTCTTTCTATATAAGTGCAGAAGAATCATGTTAAATTAAATCTACAGGGCAGG 301
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                                                                                                                                                                                                                                                                        APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OP INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8976
LENGTH: 399
                                                                                                       139 craracarririricrracrirraar 115
                                                               357 ATGTGTTTTTTTTTTAGAAT 381
                                                                                                                                                                                         US-09-621-976-8976/c
; Sequence 8976, Application US/09621976
; Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-621-976-8976
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local Simi
Matches 35;
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SRIOR PLING DATE: 2000-10-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 17305

SEQ ID NO 17305
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0
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3.8%; Score 36.2; DE
Best Local Similarity 50.3%; Pred. No. 20;
Matches 89; Conservative 0; Mismatches
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSELSEQ. for Windows Version 4.0
SEQ ID NO 12896
LENGTH: 451924
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; Patent No. 6812339
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US-09-949-016-17433
Sequence 17433, Application US/09949016
Parent No. 6812339
GENERAL INFORMATION:
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ilarity 50.3%;
Conservative
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-016-17305/c
                                                                                                                                                         TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                  US-09-949-016-12896
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US-08-998-416-224/c
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ORGANISM: Human
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Sequence 12617, Application US/09949016

Sequence 12617, Application US/09949016

Sequence 12617, Application US/09949016

SENERAL INFORMATION:
TOTAL OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PAPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 2070-12

SOFTWARE: PASTESED for Windows Version 4.0
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CLOO1307; CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PALLICATION NUMBER: 00/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTHARE: FASESEQ for Windows Version 4.0
SOFTHARE: FASESEQ for Windows Version 4.0
SEQ ID NO 17433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGCCAAAGCTGTTATGTAAAACCCTCCGGGGAATGAAATGAAATTATGTTTATACAGTT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 CAAGAAAATAGATAGGTCTGAGGATTAGGGAGCTGTTCAGTTGCTAGGAGGAACACAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 160018;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 35.8; DB 4; Length 101349;
Pred. No. 9.5;
0; Mismatches 92; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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3.7%; Score 35.6; D
Best Local Similarity 50.0%; Pred. No. 15;
Matches 89; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1) ... (160018)
CTHER INFORMATION: n = A,T,C or G
US-09-949-016-12617
                                                                                                                                                                                                                                                                                                                                                                                                                      3.8%;
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Best Local Similarity 49.7
Matches 91, Conservative
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NAME/KEY: misc_feature
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US-09-949-016-12617/c
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                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-17433
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US-09-949-016-15994/c

US-09-949-016-15994, Application US/09949016

Sequence 15994, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-0-10-03

PRIOR FILING DATE: 2000-0-10-03

SPRIOR FILING DATE: 2000-0-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeQ for Windows Version 4.0

SEQ ID NO 12994
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                                                33183 AAGGAATİCİAİTATAİTAİGGİCTATİAAĞAAATTCTĞTAİAATGAĞTAGCTİCTAİCİAT 33124
                                                                                                                                                                33123 crcrcaactricatercatacatactretetadeteretetacacadedacacetae 33064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 AGGGCAGGATTGTTGTTTTTTTTTCTCTTTCAAGCAAACTTCAGTGCTGTCAGATAACTTC 353
294 AGGGCAGGATTOTTATTTTTCTCTTTCTCAAGCAAACTTCAGTGCTGTCAGATAACTTC 353
                                                                                                                                                                                                                                                                                   33063 Trrcadrrciririririririradalagagrcicccrcrcacccaccrcradia 33006
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                                                                                                                                                                                                                            354 TCCATGTGTTTTTTTTTTTTTTTTTTAAATGAGCCCTTCCTGAGAACCCCTCGGAATAGT 411
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APPLICANT: Poblaman, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Rocchile, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89; Indels
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3.7%; Score 35.6; D
Best Local Similarity 50.0%; Pred. No. 15;
Matches 89; Conservative 0; Mismatches
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GENERAL INFORMATION: APPLICANT: Philippeen, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(160018
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US-09-949-016-15638/C

US-09-949-016-15638/C

Sequence 15638, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VANTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFREENCE: CLOOD1307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRANCE PRACES (or Windows Version 4.0)

SEQ ID NO 15638

LENGTH: 69764
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                                                                                                                                                                                                                                                                                                                                                  599 GAATCCTGCACATTTGGAGAACAACAATACTAACTCAACTGTAAATGCTGAAGTCCTTT 540
                                                                                                                                                                                                                                                                                                                                                                                                     455 ACTCACATCTGCCTCTCTCAGACACAAACCATTTCCACCTGCCAGGGCTCGGGTGTGGT 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                  539 ACCCACTTTCTCCTCACCCTGACAGAAAGGTTTACTCCCGAAATGGGTTGGGGGATGGG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 GGGTATGAAACCCTCTGCACGCCTTTTGTTGTCCATCCCTTGCCAAAGCTGTTATGTAAA 212
                                                                                                                                                                                                                                                                                                 DB 4; Length 69764;
                                                                                                                                                                                                   Score 35.2; DB 4; Length 601;
Pred. No. 0.42;
0; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515 ACAGGITICAGAGIATICACIGAAGCAGAAAT 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 GCATGAGAACAGTGCTCTTTAAAATCGTAAT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.7%; Score 35.2; DE
Best Local Similarity 54.7%; Pred. No. 12;
Matches 70; Conservative 0; Mismatches
       NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)...(69764)
COTHER INFORMATION: n = A,T,C or G
US-09-949-016-15638
                                                                                                                                                                                                   Query Match
Best Local Similarity 52.0%;
Matches 79; Conservative
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US-09-949-016-11852/c
                                                                                                                            , ORGANISM: Human
US-09-949-016-84673
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                           SOFTWARE: FastSE
SEQ ID NO 84673
LENGTH: 601
                                                                                                        TYPE: DNA
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Batent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-1755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 TGCAGAAGAATCATGTTAAATATAAATCTACAGGCCAGGATTGTTAGTTTTTTCTCCTTCTCA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 traaratraaraactraa--raarcrarrrarraaraaaarggrararraaraa 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 AGCAAACTICAGIGCIGICAGAIAACTICICCAIGIGITITITITITITICICITIAGAAIGA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 AATTAAATTAAATACTATTTAATAAATATTCTATAAGTAATTTCTTATTATTTTTATAA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.7%; Score 35.4; DB 3; Length 782; Best Local Similarity 53.6%; Pred. No. 0.44; Matches 96; Conservative 0; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                              SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC 1997
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTONNEY/AGENT INPORMATION:
NAME: Med.98, J. Timochy
REGISTRATION NUMBER: 38,241
REFERENCE/POCKET NUMBER: 38,241
REGISTRATION NUMBER: 919-541-6587
                                                  ADDRESSER: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
TITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 524: SEQUENCE CHARACTERISTICS: LENGTH: 782 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   919-541-8689
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Gaps

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58; Indels

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PAREMEL INFORMATION:

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILER REFERENCE: CLOO1307

FILER REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 321022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50388 GAATCCTGCACATTTGGAGAACAACAATACTAACTCAACTGTAAATGCTGAAGTCCTTT 50329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50328 ACCCACTITCTCTCTCACCCTGACAGAAAGGTTTACTCCCGAAATGGGTTGGGGAATGGG 50269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455 ACTCACATCTGCCTCTCTCAGACACAAACCATTTCCACCTGCGGGGCTCGGGGTGTT 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.7%; Score 35.2; DB 4; Length 321022; Best Local Similarity 52.0%; Pred. No. 34; Matches 79; Conservative 0; Mismatches 73; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50268 GCATGAGAAACAGTGCTCTTAAAATCGTAAT 50237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      515 ACAGGITICAGAGIATICACIGAAGCAGAAAI 546
Sequence 11852, Application US/09949016
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CRGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(321022)
CTHER INFORMATION: n = A,T,C or G
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Search completed: March 27, 2005, 03:59:08 Job time : 173.092 secs

Sequence 774, App Sequence 14786, A Sequence 1504, Ap

Sequence

Sequence

Sequence

Sequence Sequence

Sequence 63, Appl Sequence 27, Appl Sequence 27, Appl Sequence 31, Appl Sequence 29357, A Sequence 1312, Appl Sequence 71, Appl Sequence 6, Appl Sequence 5, Appli Sequence 1,53, Appli Sequence 1,53, Appli

Sequence 9068, Ap Sequence 57419, A Sequence 17649, A

Sequence Sequence 1

Sequence Sequence Sequence Sequence Sequence

and Antibodies

OM nucleic

Run on:

Sequence:

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TGTCCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 150
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                                               US-10-087-192-130
US-10-027-632-99132
US-10-027-632-99132
US-10-257-166-147
US-10-184-644-514
US-10-184-634-514
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US-10-741-600-17649
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Fublication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and;
FILE REFERENCE: PCO06
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM 01;
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1391
LENGTH: 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (529)
; OTHER INFORMATION: n equals a,t,g, or
US-09-764-891-1391
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OTHER INFORMATION: n equals a,t,g,
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Query Match
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Sequence 60, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 19, Appl
Sequence 11, Appl
Sequence 71, Appl
Sequence 73, Appl
Sequence 5, Appl
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Sequence 73, Appl
Sequence 600, App
Sequence 81, Appl
Sequence 1, Appli
                                                                                                                                March 26, 2005, 22:06:11; Search time 550.168 Seconds (without alignments) 10290.242 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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7 US-10-276-774-73
7 US-10-296-115-600
7 US-10-092-900A-81
3 US-10-054-691-1
8 US-10-478-245-19
8 US-10-092-900A-85
8 US-10-978-245-11
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Listing first 45 summaries
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Minimum DB Maximum DB

Database

Searched:

426

Gaps

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Indels

Length 572;

Result

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; Sequence 73, Application US/10276774
; Publication No. US20040053245A1
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Hyseq, Inc.
; TILLE OF INVENTION: NO. US20040053245A1e1 Nucleic Acids and Polypeptides
; TILLE REFERENCE: 21272-030
; FILE REFERENCE: 21272-030
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
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TITLE OF INVENTION: NO. US20040053248Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: NO. US20040053248Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: NO. US20040053248Alel Nucleic Acids and Polypeptides
CURRENT APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEC ID NOS: 1478
SEC ID NO 600
LENGTH: 802
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Sequence 600, Application US/10296115
Publication No. US20040053248A1
GENERAL INFORMATION:
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427 ATCAAGCCAGCCATTGAG 444
                                     151 ATCAAGCCAGCCATTGAG 168
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Best Local Similarity 93.6%;
Matches 73; Conservative (
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CORGANISM: Homo sapiens
US-10-296-115-600
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CORGANISM: Homo sapiens
US-10-276-774-73
                                                                                                                           RESULT 2
US-10-276-774-73
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LENGTH: 802
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2939 TGTCCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 2998
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OTHER INFORMATION: Incyte ID No: 7504684CB1
    PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/293,726
PRIOR PILING DATE: 2001-05-25
PRIOR PLING DATE: 2001-05-25
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR PLING DATE: 2001-07-06
PRIOR PLING DATE: 2001-07-06
PRIOR PLING DATE: 2001-07-26
PRIOR PLING DATE: 2001-08-24
PRIOR PLING DATE: 2002-01-22
PRIOR PLING DATE: 2002-01-22
PRIOR PLING DATE: 2002-01-22
PRIOR PLING DATE: 2002-01-22
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Shency, Suresh G.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Pena, Carol E.A.
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Lepley, Denise M.
Rieger, Daniel K.
Burgess, Catherine E.
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Fernandes, Elma R.
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Gangolli, Esha A.
Vernet, Corine A.M.
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Gerlach, Valerie
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Catterton, Elina
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Gusev, Vladimir Y.
Ji, Weizhen
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Miller, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suo, Xiaojia Sasha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Casman, Stacie J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leite, Mario W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO 19
LENGTH: 4424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-092-900A-85
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Sequence 1, Application US/20020115846A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Miranda, Maricar
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. US20020115846A1e1 Human Lipase and Polynucleotides Encoding tFILE REFERENCE: LEX-0303-USA
CURRENT APPLICATION NUMBER: US/10/054,691
CURRENT FILING DATE: 2001-01-22
PRIOR PILING DATE: 2001-01-24
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                                                                                                                                                           367 TTTTTCTCTTAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC
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                                                                                          Gaps
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        Length 4268;
                                                                                     5; Indels
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APPLICANT: YUE, Henry; AZIMZAI, Yalda;
APPLICANT: BUGGHW, MATTIAH R.; BURFORD, Neil;
APPLICANT: BAUGHW, MATTIAH R.; BURFORD, Neil;
APPLICANT: DAS, Debopriya; NGUYEN, Danniel B.;
APPLICANT: YAO, MONIQUE G.; ARVIZU, Chandra S.;
APPLICANT: GRIFFIN, Jennifer A.; ELLIOTT, Vicki S.;
APPLICANT: RAMKUMAR, Jayalaami; LAL, Preeti G.;
APPLICANT: LEE, Soo Y.; YUE, Huibin; Preeti G.;
APPLICANT: LEE, Soo Y.; YUE, Huibin; Catherine A.;
APPLICANT: YANG, Junning; TRIBOULEY, Catherine M.;
APPLICANT: YANG, Junning; TRIBOULEY, Catherine M.;
APPLICANT: YANG, Junning; TRIBOULEY, Catherine M.;
TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
Query Match
7.4%; Score 70; DB 17;
Best Local Similarity 93.6%; Pred. No. 1.2e-10;
Matches 73; Conservative 0; Mismatches 5.
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4377
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CURRENT APPLICATION NUMBER: US/10/478,245
CURRENT FILING DATE: 2003-11-18
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PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: US 60/292,242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-691-1
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Best Local Similarity
Matches 73; Conserva
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US-10-054-691-1
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111 gTTGGTAGGAGGAACACAAAAGCACAGACCCCAGACTACAATGGGTATGAAACCCTTGG 170
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APPLICANT: Famodu, Omolayo
APPLICANT: Famodu, Omolayo
APPLICANT: Hantke, Sabina
TITLE OF INVENTION: Plant Reproduction Polynucleotides and Methods of Use
TITLE OF INVENTION: Plant Reproduction Polynucleotides and Methods of Use
FILE REFERENCE: DD0010R
CURRENT APPLICATION NUMBER: US/09/967,552A
CURRENT PILING DATE: 2001-09-28
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: US 60/151,575
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 ITITICICITAGAATGAGCCCTICCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC
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4.4%; Score 41.6; DB 9; Length 5506;
Best Local Similarity 53.8%; Pred. No. 0.16;
Matches 86; Conservative 0; Mismatches 74; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70; DB 18; Length 4607;
Pred. No. 1.2e-10;
0; Mismatches 5; IndelB
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CTHER INFORMATION: Incyte ID NO: 2440624CB1
US-10-478-245-11
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/293,726
PRIOR APPLICATION NUMBER: US 60/295,346
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR PILING DATE: 2001-07-06
PRIOR PILING DATE: 2001-07-06
PRIOR PILING DATE: 2001-08-24
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2002-01-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3186 ATCAAGCCAGCCATTGAG 3203
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APPLICANT: Morgante, Michele
APPLICANT: Sakai, Hajime
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.4%;
Local Similarity 93.6%;
les 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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US-09-967-552A-73
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US-09-967-552A-73/c
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Best Local S
Matches 73
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        IITLE OF INVENTION: No. US20040043382Alel Proteins and Nucleic Acids Encoding Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.4%; Score 70; DB 17; Length 4425; Best Local Similarity 93.6%; Pred. No. 1.2e-10; Matches 73; Conservative 0; Mismatches 5; Indels (
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APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
APPLICANT: BUGGH, MATIALA R.; SURFORD, Neil;
APPLICANT: BUGGH, MATIALA R.; BURFORD, Neil;
APPLICANT: BUDGH, MATIALA R.; BURFORD, Neil;
APPLICANT: DAS, Debopriya; NGUYEN, Danniel B.;
APPLICANT: PAO, Monique G.; ARVIZU, chandra S.;
APPLICANT: TANG, MONIQUE G.; ARVIZU, Chandra S.;
APPLICANT: GRIFFIN, Jennifer A.; ELLIOTT, VICKI S.;
APPLICANT: GRIFFIN, Jennifer A.; ELLIOTT, VICKI S.;
APPLICANT: RANKUMAR, Jangalan, LEE, Ernestine A.;
APPLICANT: LIEE, Soo Y.; YUE, Hulbin;
APPLICANT: LIEE, Soo Y.; YUE, Hulbin;
APPLICANT: TANG, JUNNING; TRIBOLLEY, CATHERINE A.;
APPLICANT: TANG, JUNNING; TRIBOLLEY, CATHERINE A.;
APPLICANT: TANG, JUNNING; TRIBOLLEY, CATHERINE A.;
FILE REFERENCE: PI-0427 USN
CURRENT APPLICATION NUMBER: US/10/478,245
CURRENT FILING DATE: 2003-11-18
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-05-17
PRIOR PRILCATION NUMBER: US 60/292,242
                                                      TITLE OF INVENTION: OF USECULATORS FOR CURRENT APPLICATION NUMBER: US/10/092,900A CURRENT FILING DATE: 2002-03-07 (2014);322 PRIOR FILING DATE: 2001-03-08 (2014);322 PRIOR FILING DATE: 2001-03-08 (2014);322 PRIOR PELICATION NUMBER: USSN 60/283,675 PRIOR PELING DATE: 2001-04-13 PRIOR PELICATION NUMBER: USSN 60/234,281 PRIOR FILING DATE: 2001-12-03 PRIOR FILING DATE: 2001-13-08 PRIOR FILING DATE: 2001-03-08 PRIOR PELICATION NUMBER: USSN 60/274,191 PRIOR PELICATION NUMBER: USSN 60/274,191 PRIOR PELICATION NUMBER: USSN 60/274,191 PRIOR PELICATION NUMBER: USSN 60/274,191 PRIOR PELICATION NUMBER: USSN 60/274,191 PRIOR PELICATION NUMBER: USSN 60/274,191 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,995 PRIOR PELICATION NUMBER: USSN 60/279,9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (16)..(4285)
US-10-092-900A-85
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PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-66
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-06
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PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_22997C.1 US-10-437-963-17333
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                                                                                                                                                                                                                      FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(2339)
OTHER INFORMATION: unsure at all n locations
FRATURE:
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR FILING DATE: 2000-03-21
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Best Local Similarity 54.2%;
Matches 83; Conservative 0
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Samudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Wall, Daniel
Trawick, John
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SEQ ID NO 17333
LENGTH: 2339
TYPE: DNA
ORGANISM: Oryza sativa
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US-10-282-122A-18201/c
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
     3967 GTAACTTGAATATAAAAAACAAGTCAAAACTCATAACTGTGATGGTTAAGAACACCTATAC 3908
                                                                                                                                                                                                     3907 AACCATGCCATTGTCTATGCCAATCCAAAACTTAATTCCAAACCTAGTTGAAAGTGAA 3848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Danieuskaya, Olga
APPLICANT: Hermon, Pedro
TITLE OF INVENTION: Imprinting in Plants to Control Gene
TITLE OF INVENTION: Expression
FILE REPREBUCE: 1487
CURRENT APPLICATION NUMBER: US/10/387,894
CURRENT PILING DATE: 2003-03-13
PRIOR APPLICATION NUMBER: US 60/363,861
PRIOR PILING DATE: 2002-03-13
PRIOR PILING DATE: 2002-03-13
PRIOR PILING DATE: 2002-03-13
PRIOR FILE NOS: 6
SOFTWARE: PASELSEQ for Windows Version 4.0
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4.4%; Score 41.6; DB 16; Length
Best Local Similarity 53.8%; Pred. No. 0.27;
Matches 86; Conservative 0; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       3847 TGAAGAGAGAAAAAAAAACTTAGTATCTAACTATACA 3808
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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| LOCATION: (11384)...(11481)
| OTHER INFORMATION: N = A, T, C or G
US-10-387-894-5
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Publication No. US20030177547A1
GENERAL INFORMATION:
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ORGANISM: Zea mays
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US-09-960-352-14786

US-09-960-352-14786

Sequence 14786, Application US/09960352

Sequence 14786, Application US/09960352

Batent No. USZOOZO137139A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Byatt, John C.

TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: USG/37-21(10298)C

TITLE OF INVENTION: USG/37-21(10298)C

TITLE OF INVENTION: USG/37-21(10298)C

SEQ ID NOS: 15112

SEQ ID NO 14786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            685 CITIGACCITGGCATCCIGGGCICACAGACGTGGTIACTGCTTAGGCAGCTCAGCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           565 GGATTGGAATGTACAGAAAAGGCTCCCGGACCACGAAGCCCCCAGGATTGTCCTAACATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      625 TCTCAAGTTGCTTACCTGACGTCAGCCCCCCAAGCAGGAAGTGTCTATGGATCGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  505 CGGGTGTGGTACAGGTTTCAGTATTCACTGAAGCAGAAATGTACTTCTTACATACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17; Length 2031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 145; Indels
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                                                                                                                                                                                                                                                                                          APPLICANT: MASURO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REPERENCE: 044335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PAECHLIN VEY: 2.1
SOFTWARE: PAECHLIN VEY: 2.1
SEQ ID NO 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.0%;
                                                                                    YAMAMOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                                                     YOSHIKAWA, TSUTOMU
                                                                                                                                                                                 IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
OTSUKI, 152.
WAKAMATSU, AI
SATO, HIROYUKI
                                                                                                                                                                                                                                                 OTSUKA, MOTOYUKI
NAGAHARI, KENJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.3
Matches 125; Conservative
                                                                                                                                                               NAGAI, KEIICHI
                                                                                                                                             OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CRGANISM: Homo sapiens
US-10-094-749-774
                                                                                              ISONO, 1 YURI
                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 2, Application US/10312841

Publication No. US20030186277A1

GENERAL INFORMATION:

TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHG

TITLE REPERENCE: B01/1208/W0

CURRENT APPLICATION WIMBER: US/10/312,841

CURRENT FILING DATE: 2002-12-30

NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185535 TIGITATATGATTIGIGITAAATATATATATAAAATGGATTGTTTTTAGTTTTTT 185594
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                                                                                                                                                                                                             257 TATATAAGTGCAGAAGAATCATGTTAAATAAATCTACAGGGCAGGATTGTTAGTTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                             ö
                                                                                                                                     Score 38.6; DB 17; Length 816;
Pred. No. 0.49;
0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           publication No. US20030219741A1
GENERAL INFORMATION: APPLICANT: SUGIYAMA SUGIYAMA
APPLICANT: SUGGIYAMA, TOWNYASU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.8%;
Matches 92; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                          ; TYPE: DNA
; ORGANISM: Campylobacter jejuni
US-10-282-122A-18201
                                                                                                                                             4.1%;
Local Similarity 56.8%;
nes 71; Conservative
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; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2
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LENGTH: 3673778
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US-10-094-749-774
                                  SEQ ID NO 18201
LENGTH: 816
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                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                     Query Match 3.9%; Score 37.4; DB 9; Length 424; Best Local Similarity 53.8%; Pred. No. 0.82; Matches 77; Conservative 0; Mismatches 66; Indels (
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (373)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 63-LIB34-008-01-E1-H4
US-09-960-352-14786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: March 27, 2005, 12:55:15
Job time : 559.168 secs
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Danio rer RPCI-11-2 SP Ba006 Drosophil Danio rer Danio rer

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BX247380 AQ488455 CL7Q1048465 AL097768 BX184059 BX184059 BX184059 BX184059 BX184059 BX18405 CA792141 AA74138 AA74138 AA74138 AA74138 BA605840 CCA72132 BH487663 BE608381 BE608381 BE608381 BE608381 BE608381 BE608381

ef22g11.x USDA-FP 1

AJ741338 602325858

Drosophil LeukoS5

Mus muscu BOHGU54TF

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Run

Sequence:

Minimum DB Maximum DB

Database

Result

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Searched:

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Nume musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; EuteleoBtomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 460)

Rabael.1.0., de Jong, Malek, J., Shatsman, S., Akinret, B., Levins, M.,

Russell, D., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

Other GSSs: RPCI-24-214P9.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

Library availability, please contact Pieter de Jong

(pdejong@mail:cho.org). Clones may be purchased from BACPAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Seq primer: T7

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                              A60 bp DNA linear GSS 18-JUL-2001
RPCI-24-214P9.TV RPCI-24 Mus musculus genomic clone RPCI-24-214P9,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/clone_lib="RPCI-24"
Rhote="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db xref="taxon:10090"
/clone="RPCI-24-214P9"
                                                  CL701053
CNS002JY
BX184059
BX180731
BH009019
CN473609
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AJ741338
BG035775
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AG572132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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663
696
708
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1861
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RESULT 1
BH069515/c
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
 EM149001 TCAAAP2E57
AW752833 IL3-CT022
BI912073 603068631
B1488437 603020936
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CK950931 4090092 B
AA67588 VZ28f11.r
CC052246 WS00916.B
CC029246 WS00725.B
CK019498 AGENCOURT
BX246070 Danio rer
                                                                                    March 26, 2005, 13:10:00 ; Search time 3061.72 Seconds (without alignments) 11810.698 Million cell updates/sec
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IL3-CT022
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CC206063 CH261-122
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CC274437 CH261-132
C90343 C90343 Dict
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CC308163 TAM32-1A1
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CR612785 F
BM549919 A
                                                                                                                                                                                                                                                                  68479088
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                      34239544 segs, 19032134700 residues
                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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950
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                                                             nucleic search, using sw model
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BM549919
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BX246070
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CC206063
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 sv
                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
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Match Length DB
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gb_est2:*
gb_htc:*
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gb_est6:*
gb_gss1:*
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gb_est4:*
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265 bp mRNA linear EST 16-OCT-1997 zv97h09.rl Soares NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767777 5' similar to SW:PHIX_RABIT_Q05017 PHOSPHOLIPASE ADRAB-B PRECURSOR ;,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             746 AAGAGGGAGGAGCAGCTGGTGTGATGTGGCGTTGACTTCTTGGAAGGTGGAGGCTGAGTG 805
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/tisone_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore, B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortum (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 178.
Location/Qualifiers
partially digested male C57BL/6J
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                      Indels 19;
                                                                                                                                                                           Length 460;
                                                                                                                                                                       Score 87.2; DB 8;
Pred. No. 5.8e-14;
0; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
/clone_lib="Soares_NhHMPu_S1"
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/db_xref="taxon:9606"
                BamH1 sites using MboI DNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA418228.1 GI:2080047
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Homo sapiens
                                                                                                                                                                               9.2%;
Local Similarity 59.2%;
Les 213; Conservative
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AA418228
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AA418228
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHW, pregnant uterus NbHW, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization freaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Mamalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 491)

Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr.,

Gunaratne; P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F. pediatric Leukemia cDNA Sequencing Project (2001)

Unpublished (2001)

Lontact: Dr. Judith F. Margolin

Contact: Dr. Judith F. Margolin

Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine

1102 Bates, Mc3-3320 Houston, TX 77030, USA

Tel: 832-824-4536

Fax: 832-825-4038

Email: clones@txccc.org
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Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SalI sites of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM149001 100 Fediatric acute myelogenous leukemia cell (FAB M1)
Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAPS701, mRNA
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                                                                                                                                                                                                                                                                                                                    Length 265;
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7.4%; Score 70; DB 1; Length 265
Best Local Similarity 93.6%; Pred. No. 5.7e-09;
Matches 73; Conservative 0; Mismatches 5; Indels
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/dev_stage="pediatric 6 years"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="TCAAP5701"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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1 (bases I to S87)

1 (bases I to S87)

1 (bases I to S87)

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW752833 58-APR-2000 IL3-CT0220-031199-025-G12 CT0220 Homo sapiens cDNA, mRNA sequence.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0220-031199-025-G12&t3=1999-11-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 39
High quality sequence stop: 478.
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                                                                                                                                                                                                                                                                                                                                                             241 TGTCCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 300
lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P. Westover A. Nishiyama Y. Ohsumi T. Itoh M. Nagaoka S. SasakiN. Okazaki Y. Muramatsu M. Schneider C. Hayashizaki Y. High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORP expressed sequence tags
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                                                                                                                                                                                                                           7.4%; Score 70; DB 4; Length 491; 93.6%; Pred. No. 6.6e-09; Live 0; Mismatches 5; Indels

    587
    organism="Homo sapiens"
/mol_type="mRNA"
    /db_xref="taxon:9606"

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Homo sapiens
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Fax: +55-11-2707001
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Matches 73; Conservative
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW752833
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TITLE

COMMENT

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/unitrogen). Research described and was constructed by C. Gruber (Invitrogen). Research described by Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and Arefall and A
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Email: gapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://inage.llnl.gov
Plate: LiAM11546 row: n column: 07
High quality sequence stop: 758.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                      Gaps
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Pred. No. 7.5e-09;
0; Mismatches 5; Indels
                                                                                                 5; Indels
Score 70; DB 2;
Pred. No. 7e-09;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                   427 ATCAAGCCAGCCATTGAG 444
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Best Local Similarity 93.6%;
Matches 73; Conservative 0
Query Match 7.4%;
Best Local Similarity 93.6%;
Matches 73; Conservative
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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                                  REFERENCE
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/note="Organ: Drain; vector: pCMV-SPORT6; Site_1: Note: this is a NIH_MGC Library."
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603290988P1 NIH_MGC_118 Homo sapiens CDNA clone IMAGE:5220333 5',
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823 bp mRNA linear BST 28-AUG-2001
60020936PI NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5191712 5',
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                        Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 823)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 IGCCCACTCAGAAIGAGCCCTTCCTGAGAACCCCTCGGAAIAGIAACTACACGTACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
found through the I.M.A.G.E. Consortium/LLNL at:
plate: LLAMI1479 row: g column: 09
High quality sequence stop: 808.
Location/Qualifiers
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Pred. No. 7.6e-09;
0; Mismatches 5; Indels
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B1912651
B1912651.1 GI:16176846
                              568 ATCAAGCCAGCCATTGAG 585
                                                                                                                                                                                                              BI488437.1 GI:15327665
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Best Local Similarity 93.6%;
Matches 73; Conservative (
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                                                                                                                                                                                  mRNA sequence.
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope cns.fr, Web : www.genoscope.cns.fr
Email: seqrefégenoscope cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
nt strand cDNA was primed with a NotI-oligo(dT) and cloned
end enriched, double-strand cDNA was digested with Not I and cloned
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BX354650 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens CDNA clone CSODC023YA08 5-PRIME, mRNA sequence.
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1 (bases 1 to 921)

1 (bases 1 to 921)

1 (bases 1 to 921)

Full "Languary Cruber, C., Jessee, J. and Polayes, D. Full "length cDNA libraries and normalization Unpublished (2001)
                                                                                                                Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Life Pechnologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Parayad by: The I.M.A.G.E. Consortium (LLNL)
CNDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
NA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
place: LLMALISS3 row: o column: 22
High quality sequence start: 27
High quality sequence stop: 726.
Location/Qualifiers
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               NITHOGG http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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(bases 1 to 880)
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and directionally cloned (EcoRV site is destroyed upon

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CR612785
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AGENCOURT_6632017 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5757033
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into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                          and it belongs to a clone representative of this cluster. For more information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?s=CSODC023BA04QPl&c=1474.f. Location/Qualifiers
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/lab host="DH10B"
/clone lib="NHH MGC 118"
/note="Vector: pGWV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed
                                                                                                                                                                                                                                                                                                             /tissue type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Contact: Robert Strausberg, Ph.D.
Email: capabbe-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLMM12798 row: j column: 10
High quality sequence stop: 664.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1081)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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larity 93.6%; Pred. No. 7.9e-09;
Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                   organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5757033"
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/db_xref="taxon:9606"
/clone="CSODC023YA08"
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nes 73; Conserv
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Best Local &
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KEYWORDS
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BM923066
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cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."
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http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1661)
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/plasmid="pCMVSPORT 6"
                                                                                                                                                                          Length 1081;
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                                                                                                                                                Score 70; DB 5; Len
Pred. No. 8.2e-09;
                                                                                                                                                                                                                     0; Mismatches
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/db_xref="taxon:9606"
/clone="CS0DC023YA08"
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HTC; CNSLT_CDNA.
Homo sapiens (human)
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Matches 73; Conserv
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DEFINITION

RESULT 11 BM549919 LOCUS ACCESSION VERSION KEYWORDS REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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CK950931 872 bp mRNA linear BST 15-MAR-2004 4090092 BARC 10BOV Bos taurus cDNA clone 10BOV27_C11 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Tel: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=IL3-CT0220-150
200-070-Hg02£t3=2000-02-15£t4=1)
Seq primer: pur 18 forward
High quality sequence start: 19
High quality sequence stort: 19
High quality sequence store: 10
Location/Qualifiers
1...608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="Adult"
/clone lib="Cr0220"
/note="Organ: colon; Vector: pucl8; Site_1: Smal; Site_2:
/note="Organ: colon; Vector: pucl8; Site_1: Smal; Site_2:
Smal; A min-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, F., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 TGTCCCACTCAGAATGAGCCCTTCCTGAGAACCCCTCGGAATAAGAACTACACGTACCCC 534
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 ITTITCICITAGAAIGAGCCCTICCIGAGAACCCCCTCGGAAIAGIAACIACGCCC
                                                                                                                                                                                                       sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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91.0%; Pred. No. 6.1e-08;
tive 0; Mismatches 7;
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/db_xref="taxon:9606"
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les 71, Conservative
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/tissue_type="leavecyte"
/lab_hode="bH108"
/clone_lib="WiH MGC_118"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
/note="vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
/note="vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
/note="vector: pCMV-SPORT6; Site_1: NotI; Sprimed
non-activated adult donors. Library is oligo-dT primed
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (BcoRV site is destroyed upon
and directionally cloned insert size I.7 kb, insert size range
cloning). Average insert size 1.7 kb, insert size
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I (bases 1 to 1033)

S NIH-MGC http://mgc.nci.nih.gov/, National Institutes of Haalth, Mammalian Gene Collection (MGC)

U Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc. CONA Library Preparation: Life Technologies, Inc. CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

Location/Qualifiers

Location/Qualifiers
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IL3-CT0220-150200-070-H02 CT0220 Homo sapiens CDNA, mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 608)
                                                                                                                                  1033 bp mRNA linear EST 20-FEB-2002
-6544181 NIH_MGC_118 Homo sapiens CDNA clone IMAGE:5745887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5745887"
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5', mRNA Sequence.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                        Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048414
Email: tade@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt "-trim fasta. Vector identified
by cross match using options -minmatch 12 -minscore 18
Plate: 27 row: C column: 11
Seq primer: CCCAGTCACGACGTTGTAAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="Pooled"
/dev stage="Multiple"
/dev stage="Multiple"
/lab host="DH10B T1 phage resistant"
/clone lib="BARC 10BOW"
/note="Organ: Small Intestine; Vector: pAgen-1; Site 1:
BCORV; Site_2: Not1; Equimolar amounts of mRNA extracted
from proximal jejuuums of 18 and 21 wk old steers, and
distal ileums of 14 day old calves. proximal jejuuum
exposed to C. oncophora for 3 and 6 weeks, and distal
ileum exposed to C. parvum for 7 days"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vr28f11.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGS:1121997 5' similar to gb:M34539 FK506-BINDING PROTEIN (MCUSE); gb:X60203 M.musculus mRNA for FK506-binding protein (MCUSE); mRNA sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.5%; Score 51.8; DB 7; Length 872; 83.1%; Pred. No. 0.0017; tive 0; Mismatches 12; Indels
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                     Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                       organism="Bos taurus"
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clone="10BOV27_C11"
                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="Holstein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="Male"
    Inpublished (2004)
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Matches 59; Conserv
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AA637588/c
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3']; double-stranded cDNA was ligated to Eco RI adaptors fAATTCGGAATCCTGI, digseted with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ralph,S., Kolosova,N., Cooper,D., Butterfield,Y., Kirkpatrick,R.,
Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G., Babakaiff,R.,
Brown-John,M., Chand,S., Featherstone,R., Masson,A., Mayo,M.,
Moran,J., Olson,T., Wong,D., Friedmann,M.F., Ritland,C.E.,
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:61133
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 445.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           764 GIGIGAIGIGGCGTIGACTICTIGGAAGGIGGAGGCIGAGIGGGAGGGAACTACAATICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      884 CTTGTTTGGTTCAAGTCAATCATTCTAGTGCTGAGGATTCAGAGCCCATGGTTAATTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 GTGGGATGATGCCTGGGTCCCGGTGGCTCCATAGGCATAGTCTGAGGAGATTATCAGTTT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
1 (bases 1 to 693)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Barstead mouse myotubes MPLRB5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42.6; DB 1; Length 63
Pred. No. 0.8;
0; Mismatches 124; Indels
                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:1121997"
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                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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Similarity 48.5%;
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locanion/Qualifiers

locanism="Picea glauca"
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Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and Bohlmann,J.
The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
University of British Columbia
University of British Columbia
Unic Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
Tel: 1-604-822-028
Fax: 1-604-822-6097
Email: bohlmann@interchange.ubc.ca
Plate: W800816 row: C column: 04
High quality sequence stop: 693
POLYA=Yes.
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Best Local Similarity 53.0%; Pred. No. 1.6;
Matches 89; Conservative 0; Mismatches 79; Indels C
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 43543;
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Human phospholipase b-like polypeptide and uses thereof
Patent: WO 02062977-A 3 15-AUG-2002;
PE Corporation (NY) (US)
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AX711964.1 GI:29787749
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ACCESSION
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                                                                March 26, 2005, 11:21:05 ; Search time 4368.45 Seconds (without alignments) 11092.094 Million cell updates/sec
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                                                                                                                             1 ataatttggctgggtgcggt.....agggaaagtccctgagggga 1000
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AC05241 F
AC119056 F
AC092405 F
AC09192 F
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AC018910 F
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AP000216 H
AP001760 H
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       version 5.1.6
- 2005 Compugen Ltd.
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1000
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                                              nucleic search, using sw model
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
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Eukaryotz Buteazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryotz Buteazoa; Entera Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz Butearotz But
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Homo sapiens (human)
Homo sapiens
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DEFINITION

RESULT 2 AC022076

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

AUTHORS

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REFERENCE

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Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dinh, H.H., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Dam, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, R., Garner, P., Halle, S., Harnandez, O., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Handlon, K., Gorrell, J.H., Guezara, W., Gall, R., Harris, C., Harris, K., Harris, K., Handron, R., Holloway, C., Hollins, B., Harris, C., Hodson, A., Hogues, M., Holloway, C., Hollins, B., Harrison, E., Huber, J., Hubyk, S., Hame, J., Jackson, L.E., Jacobson, B. Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kan, U., King, L., Korvah, J., Kovar, C., Katlsson, E., Kallys, S., Khan, U., King, L., Korvah, J., Kovar, C., Lichtarge, O., Lieu, S., Lucier, R., Luna, R., Maj, J., Lozado, R.J., Lu, X., Lucier, R., Luna, R., Maj, J., Li, Z., Lichtarge, O., Lieu, C., Lulu, W., Louiseged, H., Li, Z., Lichtarge, O., Lieu, C., Lulu, R., Maj, G., Martinez, E., Mahniney, B., McLeod, M.P., Meador, M., Mayuen, N., Mahniney, B., McLeod, M.P., Meador, M., Mayuen, N., Mayuen, N., Mitcherson, E., Mace, A., Harden, M., Mayuen, N., Oviedo, R., Parimus, E., Pull, M., Quyen, N., Mayuen, N., Oviedo, R., Primus, E., Pull, L., Qulles, M., Thomas, Y., Rueris, J., Rues, M., Tabor, P., Tamerisa, K., Tang, H., Soterer, S., Scott, G., Shen, H., Shooshtari, N., Tamerisa, K., Tang, H., Svatek, A., Tabor, P., Tamerisa, M., Tamerisa, K., Ward, Morce, S., Warte, M., Tabor, P., Tamerisa, M., Tang, M., Warne, S., Ward, Moore, S., Warten, R., Ward, M., Taylor, C., Taylor, T., Talferd, B., Tamerisa, K., Tang, H., Wu, Y., Wu, Y. F., Wu, Y. F., Mun, Y. F., Mulliams, G., Milliams, G., Milliams, G., Wulliams, G., Wulliams, G., Wulliams, G., Wulliams, G., Wulliams, G., Wulliams, G., Wulliams, G., Wulliams, G., Wulliams, G., Wulliams, G., Wulliams, G., Wulliams, G., Wul
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Submitted (08-JAN-2003) Human Genome Sequencing Center, Department Submitted (08-JAN-2003) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
Center: Baylor College of Medicine
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Direct Submission
Submitted (26-JAN-2000) Human Genome Sequencing Center, Department
Submitted (26-JAN-2000) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
Submitted (07-NOV-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Aug 9, 2001 this sequence version replaced gi:13431259.
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Missouri 63108,
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Submitted (09-UUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
4 (bases 1 to 180465)
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Homo sapiens BAC clone RP11-780J6 from 2, complete sequence.
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Paulson, E., Cotton, M. and Lohmeyer, A.
The sequence of Homo sapiens BAC clone RP11-780J6
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24083 AGGCAGATTGCCCAGGAGTTGGAGACCAGTCTGAGCAACTTGGTGAAACCCTGTCTCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAACATTGTACCTGTGAAATCATCACCACAATCAAGATAAAAAATGTGTTTATCACCCAC
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 163595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                               9: contig of 2569 bp in length
6: gap of unknown length
6: gap of unknown length
7: contig of 4041 bp in length
7: contig of 4041 bp in length
7: contig of 4041 bp in length
7: contig of 3597 bp in length
7: contig of 5397 bp in length
7: contig of 5077 bp in length
8: gap of unknown length
8: contig of 9762 bp in length
9: contig of 10851 bp in length
7: contig of 10851 bp in length
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84110: gap of unknown length
163595: contig of 79485 bp in length.
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    163595
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12664:
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60406:
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2669:
4826:
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Matches 996; Conservative
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117842
17942
27704
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9184. .19468
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11407. .11443
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11888. .11997
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25312, .25464
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18640. 18831
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5116. .2530c
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20403. 20700
/rpt_family="L2"
20771. 21051
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9. .15154
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1326. .11380
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3689.
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4585.
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WECTOR: pBACG3.6
NBIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The clone sequenced to the right is AC022076. Actual start of this clone is at base position 1 of RP11-780J6; actual end is at base position 180465 of RP11-780J6.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                  Center: Washington University Genome Sequencing Center
                                                                   Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0780J06
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9614. .9917
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365. .6672
                                                      Center code: WUGSC
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Qy 781 AAAACAAAAGGATTAAAGGAGCAGAGGAGCAGGGCTTAGAAGTTAAAGGATTAAAGGAGTCA 840 By 84034 AAAAACAAAAGGATTAAAGGAGCAGAGCTTAGAAGTTAAAGGATCA 84093 Qy 841 TTAAGCCTGGAAAGGAAAACTGAGGATAATTGTGAGCTTTTCTCAAATATA 900 Db 84094 TTAAGCCTGGAAAGGACAAAACTGAGGATAATTGAGAGCTTTTCTCCAAATATA 84153 Qy 901 CAAAAGGTTATTTTTAAAACAGGCAACTGAAGAAATGAACAGGCTTTCCCAAATATA 84153 Db 84154 CAAAAGGTTATTTTTAAAACAGGCAACTGAAGAAATGAACAGGCTTACGAAG 960 Db 84214 AAAAGGTTATTTTTTAAAACGGAAAGTCCTGAGGG 98 Db 84214 AAAAGGCTTGAGGAAGTATAAGGGAAAGTCCCTGAGGG 98 Bb 84214 AAAAGACTTGAGAAGTATAAAGGGAAAGTCCCTGAGGG 84251	REBUIL 4 ACCOSOGS ACCOSOGS ACCOSOGS Homo sapiens 12 BAC F811-112R23 (Roswell Park Cancer Institute ACCOSOGS ACCOSOGS ACCESSION ACCOSOGS Homo sapiens (human) ACCOSOGS 11 GI:24431570 REFERRICO REPERRICO ACCOSOGS HOMO sapiens (human) ACCOSOGS 21 GI:24431570 REFERRICO REPERRICO ACCOSOGS 31 GI:24431570 REFERRICO ACCOSOGS 32 GI:24431570 REFERRICO ACCOSOGS 32 GI:24431570 REFERRICO ACCOSOGS 32 GI:24431570 REFERRICO ACCOSOGS 32 GI:24431570 REFERRICO ACCOSOGS 32 GI:24431570 REFERRICO ACCOSOGS 32 GI:24431570 REFERRICO ACCOSOGS 32 GI:24431570 REFERRICO ACCOSOGS 32 GI:24431570 REFERRICO ACCOSOGS 32 GI:24431570 REFERRICO ACCOSOGS 32 GI:24431570 REFERRICO ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 REFERRICO ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOGS 32 GI:24431570 AND ACCOSOG 32 GI:244	Williams, G., Williamson, A., Wieczyk, K., Wooden, S., Worley, R., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Kucherlapati, R., Weinstock, G. and Gibbs, R.
repeat_region 2912729438 repeat_region	March Match 19.14; Pack No. 3.3e-232;	OY 721 GAGAAAAAAAAAAGGGGGAATGGGGAATGGGGAATCTAAGTAACACACAGAAAAG 780

Worley, K.

REFERENCE AUTHORS TITLE JOURNAL

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AUTHORS

Worley, K

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COMMENT

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complement(1. .2004)
/note="overlaps bases 1. .2000 of clone AC140061"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (6330 . .6461)
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complement(5184...5378)
/rpt_family="AluJo"
5379...540
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ement (f.)
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complement (5641 .5742)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (5852. .6017) /rpt_family="AluSx"
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303. .337
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complement(616. .911)
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2153. .2191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STSS are identified using ePCR (Genome Res. 7:541-550) searches STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, Repeats are identified using RepeatMasker (A. Smit and P. Green, Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1s-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence flanked by consensus splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Oct 31, 2002 this sequence version replaced gi:22795134. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (27-DEC-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                       Submitted (12-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 181102)
                                                                                                                                                                                                                                                                                                                                                                 Submitted (31-CCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 181102)
                                                                                        Submitted (14-FEB-2001) Human Genome Sequencing Center, Department Submitted (14-FEB-2001) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 181102)
                                         (bases 1 to 181102)
                                                               Worley, K.C.
Direct Submission
Direct Submission
                   Jnpublished
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repeat_region repeat_region

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

/organism="Homo sapiens" Location/Qualifiers

source

FEATURES

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(E-mail:petsai@nhri.org.tw, URL:http://www.nhri.org.tw/,
Tel:886-2-28267319, Fax:886-2-28200552)
The Chimparace Chromosome 22 Sequencing Consortium consists of:
The Chimparace Chromosome Center at Shanghai, Shanghai, China;
*Chinese National Human Genome Center at Shanghai, Shanghai, China;
*GBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
of Molecular Biotechnology, Jena, Germany; *KRIBB Genome Research
Center, Daejeon, Korea;
*Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
*National Institute of Genetics, Mishima, Japan;
*National Yang Ming University Genome Research Center, Taipei,
                                                                                                                                                                                                                                                                                                                            Center: National Yang Ming University Genome Research Center Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The PTB1 chimpanzee BAC library was prepared from DNA isolated from cultured cells established from the blood of a single male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosome 22 Sequencing Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemistry, or covered by high quality data (i.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 AGA----TTGCCCAGGAGTTGGAGACCAGTCTGAGCAACTTGGTGAAACCCTGTCTTAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This entry has been annotated with sequence setfinates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reads Assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   attempt was made to resolve all sequencing problems, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 TTTGGCTGGGTGCGGTCGCTCTAATCCCAGCACTTTGGGAGGCCAAGGTAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neighboring clones: CH251-388003(left) and PTB-059114(right)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequenced with an alternate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clones may be obtained from Asao Fujiyama and co-workers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------- Summary Statistics Sequencing vector: pUC18; 100% of reads Chemistry: Dys-terminator Big Dys and ET; 100% of program: Phrap; version 0.990319
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                                                                                                                                                                                                                                                                                                         *RIKEN Genomic Sciences Center, Yokohama, Japan.
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155,086 bases at least Q30
155,086 bases at least Q20
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68.0%; Pred. No. 1e-47;
iive 0; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
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/clone="PTB=1 chimpanzee BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subclone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism≃"Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence@ym.edu.tw
------- Project Information
Center project name:The Chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://genome.ym.edu.tw/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subclone or more than one M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regions were double stranded,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Quality Assessment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.gsc.riken.go.jp)
VECTOR: pKS145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: HK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Source information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consensus quality:
Consensus quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality:
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                                                                                                                                                                                                                                                                                                                                                                                     code: XMGC
                                                                                                                                                                                                                                                                               Taiwan;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54694 CAAACAAACAAACAAACAAACAACAACAACCTGTGAAACCTTCACCAC-ATCGACATA 54636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54575 CTGTTCCCTGCCCCCACCCCAATCCCCAGCTAACCACCAATCTGCTTCTGTCACTGTA 54516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54456 TGCCTCACGTCTTTCACTTAGCATAATTTTTGAGATTCATCCACACTTTTGCATATAT 54397
                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BS000244 155086 bp DNA linear PRI 12-JUN-2004 Pan troglodytes chromosome 22 clone:PTB-070F15, map 22, complete
                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237
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Submitted (16-MAY-2003) Shih-Feng Tsai, National Health Research
Institutes (NHRI), Division of Molecular and Genomic Medicine; 128,
Yen-Chiu-Yuan Road, Sec 2, Taipei 115, Taiwan
                                                                                                                                                                                                                                                                                                                                                                               TACCAAAAATACAAAAATTAGCCGGGCATGGTGGCATGGACCTGTAGTCCCAGCTACTC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 CICCITCCIG-ICCCIACCICACACCAGGCAACCACIAACCIICTITCCAICAATA 458
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DNA sequence and comparative analysis of chimpanzee chromosome 22

Nature 429, 382-388 (2004)

(bases 1 to 155086)

Tsai,S., Liu,T., Wu,K., Liao,T. and Hsiao,K.

Direct Submission
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                             54934 GCGTATTACAAGGTCAGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCCTGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                 3 AATTIGGCIGGGIGGCICACGCCICIAAICCCAGCACTIIGGGAGGCCAAGGIAG
                                                                                                                                                                                                                                                                       GCAGATT----GCCCAGGAGTTGGAGACCAGTCTGAGCAACTTGGTGAAA-CCCTGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAGGCTGAGATGGGAGGATCACTTGAGCTCAGAGGGGTTGAGGCTGCAGTGAGCCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 -----AAGGATACAATTTAACATTGTACCTGTGAAATCATCACCACAATCAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 AAAATGTGTTTATCACCCACAGGAGTTTTCTCAGGCCCCTTGGTAATCTCTCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               459 GATTAGTTTGCATTTTTAAAAATTTTATAAAATGGGATCAAAGAGTATATACTTT---
                                                                                                              Gaps
                                                     Length 181102;
                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 ATCACACCACTACACTCCAGCCTGGGCAACAGAGCAAGACCCTGTCTCAAA
                                          23.9%; Score 2001.
69.4%; Pred. No. 9.3e-49;
Five 0; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54396 GAATAGTTGATTCCTTTTTATTGTTGAGTGT 54366
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  8978. .9258
                                                                                                           Matches 438; Conservative
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                                                     Query Match
                                                                                  Local
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AUTHORS
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30709 GGAGACTGAGGGAGGAGAATCGCTTGAAC-CCGAGAGGCGGAGGTTGCAGTGAGCCAAGA 30767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCACACCACTACACTCCAGCCTGGGCAACAGCTGTCTCAAAAAGGATACAA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The PTB1 chimpanzee BAC library was prepared from DNA isolated from cultured cells established from the blood of a single male
                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=
                                                                                  22 Sequencing Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                   Sequencing vector: DUC18; 100% of reads
Sequencing vector: pUC18; 100% of reads Assembly
Chemistry: Dye-terminator Big Dye and ET; 100% of reads Assembly
program: Phrap; version 0.990319
program: Phrap; version 0.990319
program: Phrap; version 0.990319
program: Phrap; version 0.990319
program: Phrap; version 0.990319
program: Phrap; version 0.990319
program: Phrap; version 0.990319
Consensus quality: 201,302 bases at least 020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This entry has been annotated with sequence estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neighboring clones: PTB-070F15(left) and PTB-339M13(right) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 201304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clones may be obtained from Asao Fujiyama and co-workers (https://www.gsc.riken.go.jp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an attempt was made to resolve all sequencing problems, Ecompressions and repeats; all regions were covered by at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                   Center project Information
Center project name: The Chimpanzee Chromosome
Center clone name: HL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.4%; Score 234.4; DB 9;
llarity 68.0%; Pred. No. 1e-47;
Conservative 0; Mismatches 176;
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68759. 68761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68759. .. 68761
/note="low quality region"
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|organism="Pan troglodytes"
|mol_type="genomic DNA"
|db_xref="taxon:9598"
site: http://genome.ym.edu.tw/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="22"
/clone="PTB-059114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Quality Assessment:
                                  Contact: sequence@ym.edu.tw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches 405; Conserv
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Tabil,S., Liu,T., Wu,K., Liao,T. and Hsiao,K.

Direct Submission

Submitted (16-WAY-2003) Shih-Feng Tsai, National Health Research

Submitted (16-WAY-2003) Shih-Feng Tsai, National Health Research

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The Chimparzee Chromosome 22 Sequencing Consortium consists of:

The Chimparzee Chromosome 22 Sequencing Consortium consists of:

*Chinese National Human Genome Center at Shanghai, Shanghai, China;

*CBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute

Of Molecular Boicechology, Jena, Germany; *KRIBB Genome Research
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                 77441 gakdactigakgenagakdaaticacttigaac-ccaadadgegadagtrigcagtigadgenaga 77499
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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*Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
*National Institute of Genetics, Mishima, Japan;
*National Yang Ming University Genome Research Center, Taipei,
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Homo sapiens genomic DNA, chromosome 21q22.3-ter, Ter region, clone
[E27E1-T1136, segment 2/4, complete sequence.
9834 CAAAAGTGTCCTTGTGTTCCTTGGTCCTC-CTCTCTTCGGATCCTTCTGGCTTTCCCCAT 9892
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2 (bases 1 to 100000)
2 (bases 1 to 100000)
4 (bases 1 to 100000)
Buttori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.

Direct Submission
Submitted (10-MAY-1999) Masahira Hattori, The Institute of Physiand Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattoriéggs.riken.go.jp, WRL:http://hdp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9923,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10013 ATAATTATTTTGAGATTCATTCATTCTGTATCAATAGTTTACTCCTTCTCATT 10067
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                                                                      180 AAGGCTGAGATGGGAGGATCACTTGAGCTCAGAGGGGTTGAGGCTGCAGTGAGCCGTGAT
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/map="21q22.3-ter"
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Rujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
L. Bublished Only in Database (1999)
E. 2 (bases 1 to 82117)
E. 4 (bases 1 to 82117)
E. 4 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Rujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
L. Submitted (13-MAY-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@Sc::riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Jul 17, 2001 this sequence version replaced gi:12539444.
                                                                      80828 ACATTIGIACAGCIGIGGAAAGCAICACIACAAICAAGAIAGIGACCAITAICCAGCACGC 30887
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30768 TIGIGICACTICACTCCAGCCIGGGCGATAGAGTGAGACTCCGTTCTCAAAAGTTTTAAG 30827
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Homo sapiens genomic DNA, chromosome 21q, clone:CMP21-1D4, complete
sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Submitted (10-APR-2000) The Chromosome Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Kejo University School of Medicine, Dept. of Molecular Biotechnology Genetics (addresses see below)
On May 30, 2000 this sequence version replaced gi:7717454.
On May 30, 2000 this sequence version replaced gi:7717454.
The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagamihara 228-8555, Japan,
Ohki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K., Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R., Patterson, D., Reichwald, K., Rump, A., Schillabel, M., Schudy, A., Zimmermann, W., Rosenthal, A., Kudoh, J., Shibuya, K., Kawasaki, K., Asakawa, S., Shintani, A., Sasaki, T., Nagamine, K., Mitsuyama, S., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, Reichelt, J., Kauer, G., Bloecker, H., Ramser, J., Beck, A., Klages, S., Rendiel, J., Kauer, G., Bloecker, H., Ramser, J., Beck, A., Klages, S., Rendie, K., Riesselmann, L., Dagand, B., Wehrmaeyer, S., Borzym, K., Vasro, M. Francis, F., Lehrach, H., Reinhardt, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keio University School of Medicine, Molecular Biology, * Tokyo
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* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
info.genome@gbf.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * Institute of Molecular Biotechnology, Genome Analysis,
Beutenbergstrasse 11, D-07745 Jena, Germany,
* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Max-Planck Institute for Molecular Genetics,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * Ihnestrasse 73, D-14195 Berlin, Gerr

* e.mail: info-chril@molgen.mpg.de

* URL: http://chr21.rz-berlin.mpg.de/

AL163305: Submitted (10-Apr-2000).
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* e.mail: nshimizu@dmb-med.keio.ac.jp

* URL: http://www.dmb.med.keio.ac.jp/
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forganism="Homo sapiens"
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/organism="Homo sapiens"
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* URL: http://hgp.gsc.riken.go.jp/
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Homo sapiens genomic DNA, chromosome 21q, section 104/105.
AP001760 AL163305 BA000005
AP001760.1 GI:7768687
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                                                                                                                                                                                                                                                                                                              24652 AGATCACTAGGTCAGGAGATCGAGACCATCCTGGCTAACGTGAGAACCCCATCTAC 24711
                                                                        24592 TTCGGCTGGGCGCGCTGCTACACCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGC 24651
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
Park,H.S., Toyoda,A., Ishli,K., Totoki,Y., Choi,D.K., Soeda,E.,
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Nature 405 (6784), 311-319 (2000)
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                                                                                                                                             /note="pericentrin, kendrin (KIAA0402), Accession No.
U52962"
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                100698. 100852,104559. 104699,106350. 106523, 107123. 107318,108738. 108960,109235. 109385, 110257. 110943,114631. 114875,115706. 115808, 116891. 117064,118810. 118929,119582. 119811, 121224. 121300,122537. 122675,123421. 123548, 124011. 124461)
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  .95567,96932.
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5105. .5317
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Cambridgeshire. CB10 13A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 25, 2002 this sequence version replaced gi:17154304.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations where found these are annotated as variations where differences are found these are annotated as variations where differences are found these are amonated as variations where of the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with conly a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate regions were either double-stranded or sequenced with an alternate regions were either double-stranded or sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given the feature table with their source databases: Em; EMBL; Sw;, in the feature table with their source databases: Em; EMBL; Sw;, in the feature table with their source databases: Em; EMBL; Sw; in the feature table with their source databases: Em; EMBL; Sw; in the feature chicamation can be found at the privary accession numbers given was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at the privary RPCI-11,2 constructed by the group
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Human DNA sequence from clone RP11-364B14 on chromosome X, complete
                                                                                                                                                                          Chordata; Craniata; Vertebrata; Buteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Pr:
1 (bases 1 to 143770)
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the together with a note of the overlapping clone, as we submit sequence submission variation annotation may not be found in the sequence submission only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate regions were inter double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession rumbers given in the feature table with their source databases: numbers given in the feature table with their source databases: maker was gamerated atabases can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence
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Human DNA sequence from clone RP1-167A19 on chromosome 1p32.1-33, complete sequence.
561
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                    41156 AAAGTGTACAAACTGAAAAGGTTTGACGTACATAATCATCTATGAAACCATCTCCACACT
                                                                                                        -GTACCTGTGAAATCATCACCACAAT
                                                                                                                                                                                                                                      333 CAAGATGAAAATGTGTTTATCACCCACAGAGTTTTCTCAGGCCCCTTGGTAATGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          562 TCGGIATACCAATAGTTC-GTCCCTTTTTATGGCTGAGT 599
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/map="18p"
/clone="RP11-168H23"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                         /chromosome="18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146838 CCAGGGAGGGTGGGAGGATTGCGTGAGC-CGGGGATTCGAGGCTGTAGTGAGCT 146780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146779 GTGACCGCACCATTGTACTCCAGCCTGGGTAATGGAGGAAGACCCTGTCTCAAAAAAATT 146720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146599 TGATCCTCACCCCATACTCAGGCAACCACTGATCTATTTCTGTCAGTATAGACTCATT 146540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146719 TTCATAAATGTTGACATACATACACCCCATGAACTGTCACAGTTAATACAAGAGAACAA 146660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146659 ACCCATCACCTCAAAAGTTTCCTTGTGCCCCTTTGTAACTCCTCCTCTTTACCCATCCT 146600
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
RPI-167A19 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Homo sapiens genomic DNA, chromosome 18 clone:RP11-168H23, complete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AGGCAGATT-----GCCCAGGAGTTGGAGACCAGTCTGAGCAACTTGGTGAAACCCTGT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCGGAAGGCTGAGATGGGAAGGATCACTTGAGCTCAGAGGGGTTGAGGCTGCAGTGAGCC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 ACAATTTAACATTGTACCTGTGAAATCATCACCACAATCAAGATGA-----AAAATGT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 GITTATCACCCACAGAGITTTCTCAGGCCCCTTGGTAATCTCTCCCTCCTGCTCCTTCC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGATCACACCACTACACTCCAGCCTGGGCAACAGAGCAAGACCCTGTCTCAAAAAGGAT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                           16; Gaps
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                                                                                                                                                                                                                                                                                                                                                                     Length 152037;
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                          /mol_type="genomic_DNA"
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/db_xref="Rights:RPCIP704A19167"
/db_xref="taxon:9606"
/chromosome="1"
/map="ps2.1-31"
/clone="RRP-167A19"
                                                                                                                                                                                                                                                                                                                                                                     20.9%; Score 209.4; DB 9 68.7%; Pred. No. 1.8e-41;
                                                                                                                                                        1. .152037
/organism="Homo sapiens"
                                                                                                                                    Location/Qualifiers
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AP005130.4 GI:29243380
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Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
L. Published Only in Database (2002)
2 (bases 1 to 181276)
R Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
L. Submitted (124-APR-2002) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-2S Suchiro-chou, Tsurumi *ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail:hattoridgec:riken:go:jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Mar 25, 2003 this sequence version replaced gi:22202835.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo gapiens chromosome 18, clone RP11-502P1
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Pred. No. 1.6e-40;
0; Mismatches 64
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COMMENT

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Location/Qualifiers
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19581. .24493
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                          Cooke, P., Dehrellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Hade, J., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Headford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Kann, L., Karatas, A., Klein, J., Lewaland, J.C., Johnson, R., Jones, C., Kann, L., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McGurk, A., McKernan, K., McLaughlin, J., Meldin, J., Meldin, J., McGurk, J., Norman, C.H., O'Connor, T., O'Donnell, P., Morzow, J., Najlor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Kwyman, D., Ye, W.J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Wyman, C.L., Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research 320 Charles Street, Cambridge, MA 02141, USA On May 26, 2000 this sequence version replaced gi:6751816.

All repeats were identified using RepeatMasker:
Smit, A. F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
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Center code: WIBR was seq.wi.mit.edu
Wab site: http://www.seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center project information
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3: gap of 100 bp
8: gap of 100 bp
6: gap of 100 bp
7: contig of 5824 bp in length
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20.6%; Score 205.6; DB 2; Length 181361;
Best Local Similarity 78.8%; Pred. No. 1.6e-40;
Matches 260; Conservative 0; Mismatches 64; Indels 6;

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Green, E.D.
                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
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Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
L. Published Only in Database (2002)
E. 2 (bases 1 to 183466)
E. 3 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
L. Submitted (12-MAY-2002) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi, ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriègec.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Jun 13, 2003 this sequence version replaced gi:29243375.
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Homo sapiens genomic DNA, chromosome 18 clone:RP11-502P1, complete
sequence.
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DEFINITION Papio anubis clone RP41-356H11, WORKING DRAFT SEQUENCE, 10 ordered
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                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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78933 AAACAAAAACTACTGCAAGCTTTTCACAA 78962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"
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/clone="RP11-502P1"
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                                                                                                                                                                                                                                         Homo sapiens (human)
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9737 CTCGGGAGGCTGAGGCGTGAGAATCGCTTGAACCCAG-GAGGTGGAGGTTGCAGTGAGCC 9679

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9678 GAGAICATGCCACTGGCCTCTGGCCAACAGAGCACACACACTCTCTCAAAAGAA 9619
                                     9618 CAACAACAACAAAATAATTTAAACCCAAATGTTTAATCAAG 9577
                                                                                                                                                                                                                       295 ACAATTTAACATTGTACCTGTGAAATCATCACCACAATCAAG 336
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 2134; contig of 2134 bp in length

* 2235; 4916; contig of 2635 bp in length

* 3917 5016; gap of unknown length

* 3917 7391; contig of 2375 bp in length

* 41709; contig of 2375 bp in length

* 41709; contig of 14282 bp in length

* 41709; contig of 14282 bp in length

* 41709; contig of 14282 bp in length

* 41810 56391; contig of 14582 bp in length

* 56392 56491; gap of unknown length

* 56392 56491; gap of unknown length

* 56392 56491; gap of unknown length

* 56392 56491; gap of unknown length

* 56392 56491; gap of unknown length

* 56392 56491; gap of unknown length

* 56392 12001; contig of 1778 bp in length

* 56393 1203 gap of unknown length

* 56393 1203 gap of unknown length

* 56393 1203 gap of unknown length

* 61201; contig of 21563 bp in length

* 61201; contig of 21563 bp in length

* 142513 164175; contig of 21563 bp in length

* 142513 164175; contig of 21563 bp in length

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* 142513 164175; contig of 21563 bp in length

* 142513 1641
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/note="assembly_fragment"
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March 26, 2005, 08:45:20; Search time 520.763 Seconds (without alignments) 11367.434 Million cell updates/sec
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1 ataatttggctgggtgcggt.....agggaaagtcctgagggga 1000
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Description	Abq82235 Human pho Aak89399 Human dig	Aaf30035 Human apo Ad108108 Human gen	Adl13861 Osteoarth	Add97164 Human can	Aas32707 Human gen	Aak64938 Human imm	Aal36434 Human mus	Abx59422 cDNA enco	Adj30172 Human mus	Acn45182 Human gen	Aah72843 Human cer	Ads36469 Human aut	Abk94411 DNA encod	Adl08112 Human gen	Aai62714 Human bre	Aal07036 Human rep	Acn37208 Human per
SUMMARIES	ABQ82235 AAK89399	AAF30035 ADL08108	ADL13861	ADQ97164	AAS32707	AAK64938	AAL36434	ABX59422	ADJ30172	ACN45182	AAH72843	ADS36469	ABK94411	ADL08112	AAI62714	AAL07036	ACN37208
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191	190.6	190.6	190.6	190.6	190.6	190.2	189.8	189.6	189.4	189.4	189	188.8	188.8	188.8	188.8	188.8	188.6	188.4	188.4	188.4	188.4	188.2	188.2	188.2
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dard, DNA, 43543 BP.	Human phospholipase protein encoding DNA	Human; phospholipase; enzyme; chromosome		Location/Qualifiers	replace(1573,A)		replace(1737,G) /*tag=h	rd name=	*Fag= C	≡e=	4.	*tag= d	product= "phospholipase" (note= "contains introne"		- 11	number= 1	replace(3097,C) /*t=g= f	ame=		*tag= g	/number= 1	*tag= h		.4637	/*tag≈ i	
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22891 TTAAGCCTGGAAAGGAĞAAACTGAĞĞĞATAATTGTGAĞCTĞTGACTTTTCTCAAATATA 22950
                                                                                 22951 CAAAAGGTTATTTTAAAACAGGCAACTGAAGAAAAATGAACAGGCTTGGCTTACGAAG 23010
                                                                                                                                                                                                                                                                                   Human, digestive system antigen, gene therapy, cancer, appendicitis,
ulcerative colitis, infection, Hirschsprung's disease, chronic colitis,
digestive system disorder; Meckel's diverticulum, ds.
                                                           CAAAAGGTTATTTTAAAACAGGCAACTGAAGAAGAAATGAACAGGCTTGGCTTACGAAG
                                                                                                                                                                                                                                                             Human digestive system antigen genomic sequence SEQ ID NO: 2975.
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2000US-0229287P
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GATCACACCACTACACTCCAGCCTGGGCAACAGAGCACAGACCCTGTCTCAAAAAGGATAC 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of digestive system, particularly cancer and cancer metastases.
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2199. .42237
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note= "20-841-149 probe"
eplace(42218,R)
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5328. .45347
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'note= "20-842-115 probe"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag= k
'note= "biallelic marker 20-828-311, polymorphic base C
                                                                                                                                                                                                                                                                                                                                                                      Apolipoprotein A-IV-related protein; AA4RP; human; biallelic marker; lipid metabolism; liver related disorder; obesity; diabetes; coronary heart disease; diagnosis; gene therapy; chromosome 11; ds.
                                      6001 AAAAGAAAAGAAAAACCAGAAGAAGAATCCCCAACATGATGGTTAGA 5956
297 AATTTAACATTGTACCTGTGAAATCATCACCACAATCAAGATGAAA 342
                                                                                                                                                                                                                                                                                                                          Human apolipoprotein A-IV-related protein (AA4RP) gene.
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/tag= ac

/note= primer 20-828-311.mis"

/tag= ao

/note= "20-828-311 probe"
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note= "primer 20-828-311.mis"
complement(1357. .1377)
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note= "primer 17-42-319.mis"
complement(12581. .12603)
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note= "primer 17-42-319.mis"
2335. .12359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= q
note= "primer 20-828.pu"
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note= "primer 20-828.rp"
0946. .12946
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note= "17-42-319 probe"
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2947. .12958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (1240. .1258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                        AAF30035 standard; DNA; 81001 BP.
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12959. .13469
/*tag= d
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/*tag= e
/number= 2
13478. .15210
/*tag= b
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AAF30035/c
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23435 cegcakdecreakdecadcadaarcecardaac-cedcaddecadaddrideadreaddadecada 23377

CGGAAGGCTGAGATGGGAAGATCACTTGAGCTCAGAGGGGTTGAGGCTGCAGTGAGCCGT

237 GATCACACCACTACACTCCAGGCTGGGCAACAGAGCAAGGACCCTGTCTCAAAAAGGATAC

23495 CTACTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGGCGCCTGTAATCCCAGCTACT

CTACCAAAAATACAAAAATTAGCCGGGCATGGTGGCATGGACCTGTAGTCCCAGCTACT

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The present sequence is that of the human apolipoprotein A-IV-related protein (AA4RP) gene on chromosome 11. The gene encodes a 366-amino acid protein (see AAB20103). AA4RP is differentially expressed in obese mouse models, indicating a role in lipid metabolism related disorders. It appears to be the human homologue of rat regeneration associated protein (RAP3), which is believed to be involved in liver regeneration, and is likely to have a similar function. It also shows 52% similarity to apolipoprotein A-IV, and is likely to have a similar function. The invention also provides AA4RP cDNAs (see AAF30036) and polypeptides, invention also provides for genotyphing a nucleic acid containing 1 or more of the biallelic markers. Also provided is a method for detecting a statisfical correlation between a biallelic marker allele and a statisfical correlation between a biallelic marker allele and a statisfical correlation between a biallelic marker allele and a statisfical correlation between a biallelic marker allele and a statisfical correlation between a biallelic marker allele and a biallelic marker allele and a statisfical correlation between the correlation and a statisfical correlations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phenotype and/or between a biallelic marker haplotype and a phenotype. Diagnostic methods are provided for determining whether an individual is at risk of developing a lipid metabolism related disorder and/or a liver related disorder, such as obesity, diabetes and coronary heart disease, and whether the individual suffers from such a disorder as a result of a polymorphism in the AAARP gene. AAARP DNA constructs can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding apolipoprotein A-IV-related proteins (AA4RP) and biallelic markers of AA4RP, useful for diagnosing lipid metabolism related disorders and/or liver related disorders.
                                                                                                                                                              /note= "biallelic marker 20-853-415, polymorphic base C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 199.2; DB 4;
Pred. No. 5.6e-41;
0; Mismatches 73;
                                                                                                                                                                                                                         /*tag= an
/note= "primer 20-853-415.mis"
complement(77166. .77185)
                                                       "primer 20-853-415.mis'
                                                                                                                                                                                                                                                                                     /*tag= ab
/note= "primer 20-842.rp"
                                                                                                                                                                                               complement (77059. .77077)
/*tag= an
"primer 20-853.pu"
.77057
                                                                                                          /note= "20-853-415 probe"
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                                                                                                                              replace (77058,Y)
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Local Similarity 77.5%;
les 268; Conservative (
                                                                           .77070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
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21-DEC-1999;
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                                                                             misc binding
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The invention relates to determining whether a subject has, or is at risk of developing, an abnormally low high density lipoprotein-C (HDL-C) level comprises determining whether the subject has an allelic variant of a polymorphic region from any of 27 genes (alleles listed in Table 5 of the specification). Also included are determining whether a male subject has, or is at risk of developing, an abnormally low HDL-C level, comprising polymorphic region listed in Table 5 which is associated with abnormally low HDL-C levels in males, and determining whether a female subject has, or is at risk of developing, an abnormally low HDL-C level, comprising et at risk of developing, an abnormally low HDL-C level comprising determining whether the female subject has an allelic variant of a polymorphic region listed in Table 5 which is associated with abnormally low HDL-C levels in females. The allelic variant in determining whether a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining whether a subject has, or is at risk of developing, an abnormally low high density lipoprotein-C (HDL-C) level comprises detecting an allelic variant of a polymorphic region from any of a set of
                                                                                                                                                                                                                                                                                                               Human; ds; SND; single nucleotide polymorphism;
high density lipoprotein-C; HDL-C; vascular disease; metabolic disease;
coronary artery disease; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/standard_name= "Single_nucleotide_polymorphism"
                                                                                   23316 AAAAGAAAAACCAGAAGAAGAATCCCCAACATGATGGTTAGA 23271
                                                   297 AATTTAACATTGTACCTGTGAAATCATCACCACAATCAAGATGAAA 342
                                                                                                                                                                                                                                                                                   Human gene associated with low HDL-C APOAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, SEQ ID NO 27; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
replace(123408,T)
                                                                                                                                                                                 ADL08108 standard; DNA; 188971
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                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-214170/20.
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                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mccarthy J;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
variation
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61 AGGCAGAT----TGCCCAGGAGTTGGAGACCAGTCTGAGCAACTTGGTGAAACCCTGTCT

ATAATTTGGCTGGGTGCGGTGGCTCACCCTCTAATCCCAGCACTTTGGGAGGCCAAGGT

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subject has, or is at risk of developing, an abnormally low HDL-C level is APOA 1 CC, CD14 1 CT, COLSA2 1 GG, EDNRB 1 AG or AA, FABP3 1 CT, GBE1 1 AG or GG, LIPC 5 AA, MTHFR 1 CC, VWF 2 GG, or their complements. The allelic variant in determining whether a male subject has, or is at risk of developing, an abnormally low HDL-C level, LRP1 3 CC or CT, PAI2 4 GG, or PPARG 1 CG, or their complements. The allelic variants are also COLSA2 1 GG, CD14 1 CT or CC, and FABP3 1 CT, in combination, or their complements. The methods are useful for diagnosting (a predisposition to) abnormally low levels of low high density lipoprotein-C (HDL-C) in a prognosticating diseases and disorders associated with abnormal lipid levels such as vascular and metabolic diseases, e.g., coronary artery diseases. The present sequence is a human gene containing a SNP (single must) contained by the present sequence is a human gene containing a SNP (single must) contained the prognosticated with low high density lipoprotein-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 188971 BP; 53091 A; 44581 C; 42653 G; 48646 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67685 AAAAGAAAAGAAAACAAAGAAGAATCCCCAACATGATGGTTAGA 67730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             joint space narrowing; osteophyte development; joint pain; osteoarthritis; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 199.2; DB 12; Learner Pred. No. 7.9e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osteoarthritis-associated polymorphic nucleotide #393.
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Best Local Similarity
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96778 TGGCCTGGAGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGTGG 96837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96957 AGGCTGAGGTGGAAĞAATCGCTTGAACCTGGAGAGGCAGAGGTTGCAGTGAGCCGAGAAT 97016
                                                                                                                                                                                                                                  The invention relates to a method of determining susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain comprising identifying whether the individual has at least one polymorphism in a polymucleotide encoding at least one of the protein listed in the specification. The methods, composition and agent are useful for modulating the susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain that is associated with a disease, preferably osteoarthritis. The cell line and the non-human animal are useful for screening for an agent for diagnosing an individual having susceptibility to joint space narrowing and/or osteophyte development and/or joint pain. This sequence corresponds to the polymuclostide encoding a protein listed in the specification. (Note: The sequence data for this parent did not form part of the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                    Determining susceptibility of an individual to joint space narrowing, osteophyte development and/or joint pain comprises identifying whether the individual has at least one polymorphism in a polymucleotide encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGCC-----CAGGAGTTGGAGACCAGTCTGAGCAACTTGGTGAAACCCTGTCTAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97017 ACACCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTCTGTCTCAAAAAATAAA 97071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96838 ATTGCCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96898 TAAAAATAC-AAAATTAGCTGGGCATGGTGGCAAGCACCTGTAATCCCAGCTACTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 TGGCTGGGTGCGGTGGCTCACGCCTCTAATCCCAGCACTTTGGGAGGCCAAGGTAGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CAAAAATACAAAAATTAGCCGGGCATGGTGGCATGGACCTGTAGTCCCAGCTACTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 154681 BP; 41177 A; 36356 C; 36934 G; 40214 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCTGAGATGGGAGGATCACTTGAGCTCAGAGGGTTGAGGCTGCAGTGAGCCGTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ACACCACTACACTCCAGCCTGGGCAACAGAGCAAGACCCTGTCTCAAAAAGGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 197; DB 10; Length 154681;
Pred. No. 2.7e-40;
0; Mismatches 40; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences).
                                                                                                                                                                                             Disclosure; SEQ ID NO 393; 297pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 84.1%;
Best Local Similarity 84.1%;
Matches 248; Conservative 0
  Schafer A;
  Jones KA,
                                                                                                                                                  a protein.
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides,

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Matches 251;
                                                    Morris DW,
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                                             AAX54951 to AAX64702 encode the human immune/haematopoietic antigen (I)
anino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polymucleotides may be used to produce the secreted (I), by inserting the
nucleic acids into a host cell and culturing the cell to express the
charges and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
concers from the present human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54912 to AAK54950 and AAM82169
represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                         9
useful for preventing, diagnosing and/or treating cancers and metastasis
                                                                                                                                                                                                                                                                                                                                                                        1 ATAATTTGGCTGGGTGCGGTGGCTCACGCCTCTAATCCCAGCACTTTGGGAGGCCAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                            AGGCAGATTGCC ---- CAGGAGTTGGAGACCAGTCTGAGCAACTTGGTGAAACCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCGGAAGGCTGAGATGGGAGGATCACTTGAGCTCAGAGGGGTTGAGGCTGCAGTGAGCC
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                                                                                                                                                                                                                                                                                                                                                Gaps
                        Disclosure; SEQ ID NO 21882; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                          Sequence 4583 BP; 1269 A; 1249 C; 1011 G; 1054 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                               Query Match
19.4%; Score 194.4; DB 4; Length 4583;
Best Local Similarity 79.1%; Pred. No. 3.2e-40;
Matches 258; Conservative 0; Mismatches 61: Indela 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cancer associated sequence HDI-08-009, SEQ ID 140.
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ID ADQ97164 standard; DNA; 145985
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treating
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                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 145985 BP; 40325 A; 30740 C; 31191 G; 43391 T; 0 U; 338 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29357 TAAAAATACAAAAAATTAGCCGGGCATGGTGGCGAGGTGCCTGTAATCCCAGCTACTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 AGAT----TGCCCAGGAGTTGGAGACCAGTCTGAGCAACTTGGTGAAACCCTGTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CAAAAATACAAAAATTAGCCGGGCATGGTGGCATGGACCTGTAGTCCCAGCTACTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 AGGCTGAGATGGGAGGATCACTTGAGCTCAGAGGGGTTGAGGCTGCAGTGAGCCGTGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.4%; Score 194.2; DB 12; Length 145985; llarity 81.2%; Pred. No. 1.4e-39; Conservative 0; Mismatches 53; Indels 5; G
                                                                                                                                                                                        New isolated cancer associated nucleic acids comprising at least contiguous nucleotides, useful for diagnosing, preventing and/or cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genomic DNA for novel endocrine antigen, SEQ ID No 661
                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 140; 199pp; English
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(SAGR-) SAGRES DISCOVERY
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                                                          Malandro MS;
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Ruben SM;
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    The invention relates to cDNAs encoding novel human endocrine antigens or a fragment having biological activity, a domain, an epitope, full length protein, variant, allelle variant or a species homologue of the convention. The DNAs and polypeptides are useful for preventing, treating or ameliorating a medical condition when administered (e.g. by coding for the antigens etherapy). Identifying mutations in the genes coding for the antigens is useful for diagnosing a pathological condition or a susceptibility to a pathological condition. The DNAs, antigens and and/ or prognosing disorders related to the endocrine system or hormone imbalance or reproductive disorders, cancers of endocrine tissues, and/ or prognosing disorders related to the endocrine system or hormone imbalance or reproductive disorders, cancers of endocrine tissues, disorders of the pancreas (e.g. diabetes mellitus), the adrenal glands (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the chycothalamus and testes (e.g. vanishing testes syndrome), many examples of diseases and disorders are given in the specification. The present cof diseases and disorders are given in the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences
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             Isolated polypeptide for treating, preventing and prognosing disorders related to the endocrine system including endocrine disorders, reproductive disorders, and gastrointestinal disorders and also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5293 GGGCGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6268 BP; 1589 A; 1498 C; 1506 G; 1675 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 19.3%; Score 193.4; DB 4; Length 6268; Best Local Similarity 79.0%; Pred. No. 6.6e-40; Matches 244; Conservative 0; Mismatches 61; Indels 4;
                                                                                    Disclosure; SEQ ID NO 661; 558pp; English.
                                                         testing and detection e.g. diagnosis.
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Rosen CA,

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(HUMA-) HUMAN GENOME SCI INC

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

camino acid sequences given in AAM82170 to AAM1921. (I) have cytostatic

activity, and can be used in gene therapy and vaccine production. (I)

corrections and polynucleotides may be used in the prevention, diagnosis and

corrections and polynucleotides may be used in the prevention. Giagnosis and

corrections and polynucleotides may be used in the prevention. For

creatment of diseases associated with inappropriate (I) expression. For

creatment of diseases associated with decreased

creatment they may be used to treat disorders associated with decreased

creativity of (I) by expressing inactive proteins or to

cuplement the patients own production of (I). Additionally, (I)

cuplement the patients own production of (I). Additionally, (I)

cuplement into a host cell and culturing the cell to express the

creative and cancer metastases of haematopoietic-derived cleases, especially

diagnose and treat immune/haematopoietic-derived cells. AAK64703

creates and cancer metastases of haematopoietic antigen genomic

to AAK87694 represent human immune/haematopoietic antigen genomic

creates and cancer metastases of haematopoietic antigen genomic

croacers from the present invention. AAK54912 to AAK54950 and AAM82169

createsers and cancer metastases.
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                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATAAITITGGCTGGGTGGCTGACGCCTCTAAICCCCAGCACTTTGGGAGGCCAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19183 BP; 5489 A; 3882 C; 4034 G; 5778 T; 0 U; 0 Other;
                                                                                                                                     Disclosure; SEQ ID NO 19750; 3071pp + Sequence Listing; English.
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19.3%; Score 193; DB 4; Length 19183;
Best Local Similarity 79.2%; Pred. No. 1.3e-39;
Matches 243; Conservative 0; Mismatches 60; Indels 4;
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                                       WPI; 2001-483426/52.
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